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3: /cgn2_6/ptodata/1,

4: /cgn2_6/ptodata/1,

5: /cgn2_6/ptodata/1,

6: /cgn2_6/ptodata/1,
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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463.411 Million cell updates/sec
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US-09-045-583-52
US-09-544-984A-2
US-08-461-244-3
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ALIGNMENTS

RESULT 1 US-09-087-232A-13

Patent No. 6153431

GENERAL INFORMATION:

APPLICANT: Quillor

TITLE C.

TITLE OF INVENTION: HUMAN IMPORTATION OF INVENTION: VARIANTS NUMBER OF SEQUENCES: 23

HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR VARIANTS ASSOCIATED WITH RESISTANCE TO V.

TO VIRUS INFECTION

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                                                                                                                         ; MOLECULE TYPE: protein US-09-087-232A-13
                                                                                                                                                      TELEFAX: (212) 765-2519
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                              Query Match
Best Local Similarity
Matches 352; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                            NAME: KOLE, LISA B. REGISTRATION NUMBER: 35,225
REGISTRATION NUMBER: APTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                         APPETCATION NUMBER: 60/048,057
FILING DATE: 30 MAY 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/087,232A FILING DATE: 28 MAY 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: New York
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New York
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Pred. No. 2.7e-144;
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RESULT 2
US-08-861-105-14
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 0
FILING DATE: 19-JUN-1996
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ADDRESSEE: David A. Jackson,
                                                                                                                      TELEPHONE: 201-487-5800
                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., Davi
                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                            NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0 FILING DATE: 13-APR-1994
                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 436
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TOPOLOGY: 11
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                                 amino acid
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US-08-861-105-14
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Patent No. 6265184
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                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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HYPOTHETICAL: N
ORIGINAL SOURCE:
                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: No. 6265184and, Gr
REGISTRATION NUMBER: 35,
                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acid
                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 206-485-1900
                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                     TOPOLOGY:
                                                                                                                                         TELEPHONE:
                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                      CLASSIFICATION: 435
                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Chicago
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                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Marshall, O'Toole, Gerstein, Murray & 6300 Sears Tower, 233 S. Wacker Drive
                                                                   352 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                             206-485-1662
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Pred. No. 2.7e-144;
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TITLE OF

TYPE:

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: .NAME/KEY: mlsc_feature
: OTHER INFORMATION: /- US-08-575-967A-2
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WOLECULE TYPE:
US-08-833-752-5
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GENERAL II
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Best Local Similarity
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                                                                                            REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SAMSON, MACHINE APPLICANT: PARMENTIER, MARC
APPLICANT: VASSART, GILBERT
APPLICANT: LIBERT, FREDERICK
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                      SOPTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA
APPLICATION NUMBER: -05/08/833,752
FILING DATE 9-APR-1997
                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                   CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Dandel E
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
ZIP: 92660
                                          TOPOLOGY:
                                                                          LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                              SSEE: Knobbe, Martens, Olson & Bear T: 620 Newport Center Drive 16th F Newport Beach
                                                       amino acid
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Pred, No. 2.7e-144;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   16th Floor
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; MOLECULE TYPE:
; FRAGMENT TYPE:
US-09-045-583-52
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US-09-045-583-52
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Best Local
                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/045,583
ETILING DATE: 20-MAR-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION: APPLICANT: Graham
                                                                         TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                             NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MN
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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                                        TOPOLOGY:
                                                               LENGTH:
                                                                                                                  TELEPHONE:
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             peptide
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No. 6287805el Molecules
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Pred. No. 2
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US-09-534-185-52
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; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-534-185-52
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Sequence 52, Application vo...

Sequence 52, Application vo...

GENERAL INFORMATION: Gerard J. et al.

APPLICANT: Graham, Gerard J. et al.

APPLICANT: OF INVENTION: No. 6403767el Molecules of the
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                                                                                                                  INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                  FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                              PRIOR
                                                MOLECULE TYPE:
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FILING DATE: 24-Mar-2000
CLASSIFICATION: <Unknown>
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                                                                                  TYPE: amino acid
                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: MNI-044
                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                            FILING
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                                                                  TOPOLOGY:
                                                                                                                                                                                                                                        NAME: Mandragouras, Amy E
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                                                                                                LENGTH: 352 amino acids
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US-08-466-343D-2
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Matches 3
                          Query Match
                                                                                                                                       TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: LI, Y1
TITLE OF INVENTION: I
TITLE OF INVENTION: (
NUMBER OF SEQUENCES:
                                                                                                                                                                 REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Rel
                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                     MOLECULE TYPE:
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                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                            LENGTH:
                                                                                                                                                                                                                          NAME: STEFFE,
                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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Score 1826; D
Pred. No. 4.6e
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Pred. No. 8.3e-144;
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US-09-517-605-5
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Patent No. 6391567
                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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APPLICANT: Kwon, Douglas S.
APPLICANT: van Kooyk, Yvette
APPLICANT: Geijtenbeck, Tneo
TITLE OF INVENTION: CELLS
FILE REFERENCE: 1049-1-017
                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/517,605 CURRENT FILING DATE: 2000-03-02
                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 352
TYPE: PRT
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                                                                                                                                               LLTIDRYLAVVHAVFALKARTVTEGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS
                                                                                                                                                                                                                                      MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFYGNMLVILILINCKR 60
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    GEKFRNYLLVFFQKHTAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL
                           HFPYSQYQFWKNFQTLKIVILGLVLFLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI 240
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nilarity 98.3%;
Conservative
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Pred. No. 4.5e-142;
3; Mismatches 3;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT: Derk B
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APPLICATION NUMBER: US/0

FILING DATE: October 3,

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270 5024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: William T. Han
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: DISKETTE,
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                                                                                                                                                                                                                                                                                                                                                                                                TYPE:
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OPERATING SYSTEM: WINDOWS
SOFTWARE: MICROSOFT WORD
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ZIP: 19406-0939
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                                                                  TIMIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYA 298
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                                                                                                                                                       IILLTIDRYLAIVHAVFALKVTTVNFGVITSVVTWVVAVFASLPEIIFTRSQKEGFHYTC
                                                   AIMIVYFLFWTPYNIVLLLTTFQEFFGLNNCSSSNRLDQAMQATETLGMTHCCLNPVIYA
                                                                                                      SPHFPHTQYHFWKSFQTLKMVILSLILPLLVMIICYSGILHTLFRCRNEKKRHRAVRLIF
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ilarity 81.4%;
Conservative 2
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Pred. No. 5.1e-120;
9; Mismatches 35;
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Best Local Similarity
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TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: FEITATO, Gregory D.
REGISTARTION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM:
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New Jersey
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VFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL
                                  VFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
                                                                                        PYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL 309
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                                                                    PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS
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Rosen, Craig A.
VVENTION: HMAN G-PROTEIN RECEPTOR HGBER32
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 4.7e-105;
2; Mismatches 46;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
ATTORREY/AGENT INFORMATION:
NAME: CSETT, Luann
REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 415-8857-0663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                        198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT
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amino acid
VFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
                  VFFQKHIAKRFCKCCSIFQQEAPERASSYYTRSTGEQEISVGL 352
                                                                     PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS
                                                                                     PYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL
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Pred. No. 4.9e-105;
2; Mismatches 46;
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RESULT 13
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US-08-446-669-4
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Patent No. 6132987
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Best Local Similarity
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TELEX: 380816CooleyPA
INFORMATION FOR SEQ ID NO: 4:
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LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC competible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Charo, Israel APPLICANT: Coughlin, Sha
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                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 259
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (617)742-421
INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
LENGTH: 360 amino acid
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                                                                                                                                                                                                                                                                                                Local 259;
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                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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                 VFFQKHIAKRFCKCCSIFQQEAPERASSYYTRSTGEQEISVGL 352
                                               PYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL 309
                                                                                                Massachusetts
VFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL
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Pred. No. 4.
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4.9e-105;
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RESULT 14 US-09-534-185-50 ; Sequence 50, Ap

Application US/09534185

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GENERAL INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Graham, Gerard J. et al.
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptahelical Receptor Superfamily and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
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FRAGMENT TYPE:
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318
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59; Conservative
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FILING DATE: 24-Mar-2000
CLASSIFICATION: <Unknown>
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STREET: 28 State Street
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                                                                                                                                 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----RG 197
                                                                                                                                                                                                                                                                    LNLAISDLLELITLPLWAHSAANEWVFGNAMCKLETGLYHIGYFGGIFFIILLTIDRYLA
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VFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
                                VFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
                                                                  PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAEVGEKFRRYLS
                                                                                    PYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL 309
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internal
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RESULT 15

Search completed: June Job time: 37.3492 secs

2003, 15:23:37

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MOLECULE TYPE:
PCT-US95-00476-4
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIF: 30012 FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: The Regents of the University of California TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT TITLE OF INVENTION: PROTEIN RECEPTORS NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: BETLING. 20,121
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 555
REFERENCE/DOCKET NUMBER: 555
TELECOMMUNICATION INFORMATION:
310-977-1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Berliner, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Robbins, Berliner & Carson
STREET: 201 N. Figueroa Street, 5th Floor
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 310-977-1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
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                                                                                                                                                                                                 130 VYHAVFALKARTYTEGVYTSVITWYVAVFASLEGIIFTRSQKEGLHYTCSSHEPYSQYQF 189
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 318
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 VFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
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Listing first 45 summaries
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Human CCR5. Homo Human chemokine re Human CC chemokine HIV-1 co-receptor Human HIV-1 co-rec protein Human HIV-1 co-rec protein Human CRS protein Human CRM protein-Human chemokine re Human Chemokine (C Human CC chemokine
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3	AAW51744	19	355	51.2	942.5
-recept	AAW88238	20	215	52.0	958
กับเกลก	AAW27408	18	215	52.0	958
ctive human CC	AAW27406	18	184	•	958
റ	AAW29179	18	355	•	1016.5
ი ე	AAB20571	21	355	57.3	1055
MIP-la	AAW25751	18	355	•	1055
an MIP-1 al	o	18	355	57.3	1055
hemok in	AAR52749	15	355	•	1055
MCP-1	AAB46859	22	329	•	1138.5,
CCR2a pro	AAG80107	22	374	•	1224
monocyte	AAR79165	16	374	•	1224
ndogenous 1	ABB56340	22	360	•	1358
_	AAU07614	22	360	•	1364
ccR2b pro	AAG80108	22	360	•	1364
monocyte	AAW35833	18	360	•	1364
monocyte	AAR79166	16	360	74.1	1364
CCR2-641	AAU07613	22	360	•	1365
CC-CKR5 pr	AAW54037	19	354	٠	1546
င္	AAW26766	18	332	•	1641.5
ue che	AAW27125	18	352	•	1807
acid seque	AAG79089	22	352	•	1814
G-protein	AAU97150	23	352	٠	1826
G-protein	AAE07046	22	352	99.2	1826
G-protein	AAE07037	22	352	•	1826
G-protein	AAY80128	21	352	•	1826
G-protein	AAW07602	18	352	•	1826
G-protein	AAU97152	23	352	•	1833
HDGNR10 p	AAB46858	22	352	•	8
G-protein	AAE07048	22	352	99.6	w
G-protein	AAE07039	22	352	•	83
n cck5 Gln	AAM52829	23	352	•	ω
pobn	ABB56342	22	352	99.7	1835
an CC chemok	2383	19	371	•	w
Fusion protein con	AAY41280	20	439	100.0	1841

ALIGNMENTS

andard; Protein; 352 AA. (first entry) ys chemokine receptor 5; Codeficiency virus; type 1; treatment; prevention; viceathic pulmonary fibrosis erosclerosis; autoimmune dis. 2. 3. 96EP-0870102. 96EP-0870021. OSCREEN SA.	DI Libert F				XX							KW asthme			KW human		DE Human CCR5.	DT 14-APR-1998	××	AC AAW27407;	AAW27407 ID AAW274
st entry) st entry) st entry) st entry) st entry) st entry) stency virus; type 1; type 2; ent; prevention; ent; prevention; ent; prevention arthritis; g; c pulmonary fibrosis; psorian c pulmonary fibrosis; psorian erosis; autoimmune disorder. erosis; autoimmune disorder. ED-0870021. N SA.		·) EUROSCREE				-1997.	019-A2	•	apiens.	•	; atheroscl	ı; idiopathi	matory dise	osis; treatm	immunodefic	Cys-Cys che	CCR5.			07;	07 standard
; 352 AA. cceptor 5; CCR5; us; type 1; type 2; ention; atthritis; ginatoid fibrosis; psoriar ry fibrosis; psoriar utoimmune disorder. 2. 2. 3.		SA.	EP-0870021	EP-0870102	#O-BE00043						erosis; au	c pulmonar	ase; rheum	ent; preve	iency viru	mokine rec		st entry)			l; Protein;
type 2; type 2; ritis; g; risorder.			٠	•	٠						toimmune d	y fibrosis	atoid arth	ntion;	s; type 1;	eptor 5; 0					352 AA.
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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Active
useful
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                                                                                                                                                                                                             Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour; asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy; diagnosis; leukocyte trafficking; g protein coupled receptor; ligand; modulator; antibody; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune disease
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                                                                                Domain
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                                                                                                                                                                                                                                                                                                                                             receptor 88C
                           /label= Extracellular_domain
56..67
                                                                                                      Location/Qualifiers
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prevent and/or treat inflammatory
and viral infection
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Pred. No. 3.6e-200;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
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20-DEC-1995;
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N-PSDB; AAT85161.
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 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV
                      LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII
                                                                                                                                                                     MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR
                                                                                                                                                                                                                                                                                          abnormal haematopoietic processes etc
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nilarity 100.
Conservative
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/label= E
125..145
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Pred. No. 3.6
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CC chemokino
                                                 Claim 68; Fig 1C; 70pp; English.
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Fong Y, Kennedy PE, Murphy
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                                                                                   CC chemokine receptor 5 polypeptide - fusion between HIV and a target cell
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DB; AAT76920.
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                                                                                                                                                                                                                                           HEALTH & HUMAN SERVICES
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/note= "transmembrane
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 comprises of a novel human macrophage-selective that has been designated CCR5. The sequence
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phy PM;
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HIV; CD4; AIDS; therapy;
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                                                                                                                                                                                                       Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR
                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
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nilarity 100.0%;
Conservative 0
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101
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67..87
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/note= "transmembrane domain
                                                                                                   /note-
                                                                                                                                                                                                     Location/Qualifiers
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                                                                                "corresponds to TGA (Stop) in (
                                                                                                                                   "transmembrane domain 2"
              *transmembrane domain
                                                                                                                                                                    "transmembrane
                                                                                                                                                                                                                                                                                           co-receptor; infection;
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Pred. No. 3.6e-200;
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                                                                                  CCr5m303"
                                                                                                                                                                     domain
                                                                                                                                                                                                                                                                                           diagnosis;
                                                                                                  in wild-type CCR5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 (M-tropic) strains of HIV-1. The invention relates to the identification of a CCR5 variant (see AAW88231), designated CCR5m303, comprising the first two transmembrane domains of wild-type CCR5, but lacking transmembrane domains 3-7. The presence of the CCR5m303 variant with the wild type CCR5 allele shows a positive correlation with resistance to infection with M-tropic HIV-1 correlation and may indicate slower progression of the disease. The detection of CCR5 variants may be used to identify individuals at lower risk of infection relative to the general population who, if infected, may exhibit slower progression to AIDS. Probes and primers (see AAV84127-36) are provided for use in diagnostic methods for detecting the presence of such variants. A method is provided for inhibiting HIV-1 infection of a cell expressing the CCR5 variant into the cell, thereby reducing the number of functional CCR5 molecules present on the cell surface.
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New CCR5 variant protein developing resistance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-1997;
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                                                MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV
                                                               MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV
                                                                                                           HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI
                                                                                                                          HFPYSQYQFWKNFQTLKIVILGLVLPLLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI
                                                                                                                                                                         LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS
                                                                                                                                                                                        LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the HIV-1 co-receptor - useful in CCR5-expressing cells to HIV-1 infection
                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                              Score 1841; DB 20;
Pred. No. 3.6e-200;
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(FORS/)
                                                                                                                                                                                                                                                                                                                                           inflammation; autoimmune disease; metastasis; bronchial asthma; lupus; chronic bowel inflammation; rheumatoid arthritis; cytostatic; antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
                                                                                                                                                                   useful for detecti
ligand inhibitors
                                                                                                                                                                                                                                                        31-MAR-2000; 2000DE-1016013
                                                                                                                                                                                                                                                                        02-APR-2001; 2001WO-EP03708
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG80111 standard; Protein; 352
                                                                                                                                                    Disclosure; Page 10;
                                                                                                                                                                                                   WPI; 2001-626256/72
                                                                                                                                                                                                                  Forssmann W, Adermann
                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                      antirheumatic;
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                                                                                                                                                                          agent containing detecting tumors,
                                                                                                                                                                                                                                                                                                                                                                    tumour diagnosis; colorectal; prostatic;
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inflammation etc., also therapeutic u
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where the (cardio)vascular, lymphatic, respiratory, nervous, digestive, endocrine, motor or urogenital systems or skin are affected, and bone marrow diseases. The products of the invention are chemokine derivatives which have cytostatic, antiinflammatory, antiasthmatic, immunosuppressive, dermatological, antirheumatic, antiarthritic. Chemokines act on specific tumor and inflammatory cells through a constellation of chemokine receptors (CR), which control migration and proliferation of these cells. AA680045-AA680128 represent human chemokine This invention describes a novel diagnostic agent (A) comprising at least two different ligands (I) for receptors (II) that are implicated in disease. (A) are used for the diagnosis of tumors (especially colorectal or prostatic), organ rejection, inflammation and autoimmune diseases. Also inhibitors of (I) are used therapeutically against tumors (and their metastases), inflammation (particularly bronchial asthma or chronic bowel inflammation), or autoimmune diseases (rheumatoid arthritis or lupus), Sequence used A ç illustrate the method of the invention.

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LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII

LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII

MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLFPLYSLVFIFGFVGNMLVILILINCKR

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Query Match Best Local (Matches

Similarity

100.0%; llarity 100.0%; Conservative 0

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Score 1841; Pred. No. 3.6); Mismatches

e 1841; Db 22, No. 3.6e-200;

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19-MAY-2000;
07-FEB-2001;
The present sequence is that of human HIV-1 co-receptor CCR5. Amino acids 2-18 in the N-terminal region of CCR5 comprise an HIV-gpl20-binding site that determines the specificity of the interaction between CCR5 and HIV-1 gpl20. Post-translational sulfation of the tyrosine residues in the CCR5 N-terminus is required for gpl20 binding and may critically modulate the susceptibility of target calls to HIV-1 infection in vivo. The invention provides claimed sulfated peptides (see AAB82947) that are based on the CCR5 N-terminal region and which are effective for inhibiting HIV-1 binding to CCR5. These peptides are used in claimed methods of inhibiting HIV infection of CD4+ cells, of preventing CD4+ cells from becoming infected with HIV, of treating
                                                                                                                                                                                                                                                                                                (PROG-)
                                                                                                                                                                                        Novel compounds comprising specific amino acids within CCR5 (HIV 1 co-receptor) amino terminal domain including negatively charged and sulfated tyrosine residues is useful for treating HIV infection in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIV-1;
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                                                                                                                                                       Claim 1; Page 30;
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AARON DIAMOND AIDS
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; 2000US-205839P.
; 2001US-267231P.
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; therapy; vaccine; anti-HIV-1.
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Matches
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                                                                                                                                                                                                                                                                                                                           a subject whose CD4+ cells are infected with HIV, and of identifying an agent which inhibits binding of a CCR5 ligand to a CCR5 receptor. The methods may be carried out in a subject, especially a human, infected (therapeutic method), not infected with HIV (prophylactic method), or in a subject who is not infected with, but has been exposed to, HIV.
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             GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL
                     GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL
                                                               MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV
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Pred. No. 3.6e-200;
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RESULT 7
AAB83354
12-JAN-2000;
12-JAN-2000;
12-JAN-2000;
                                               (PFIZ )
                                                                                                                 EP1118858-A2
                                                                                                                                                                                      AAB83354;
                                                                                          03-JAN-2001;
                                                                                                      25-JUL-2001
                                                                                                                              Homo sapiens
                                                                                                                                           human
                                                                                                                                                 Chemotactic
                                                                                                                                                             Human CCR5 protein
                                                                                                                                                                          09-OCT-2001
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                                                                                                                                          immunodeficiency
                                               PFIZER
PFIZER
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2000GB-0000661.
2000GB-0000663.
                                                                                          2001EP-0300020
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                                   Rickett
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                                   G.
                                                                                                                                         r 5; gp120; CD4; therapy; HIV; CCR5;
anti-inflammatory disease; human.
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WPI; 200 N-PSDB;

2001-477088/52. DB; AAF87099.

Determining incubating i

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an modulate CCR5-gp120 interaction, CCR5 and gp120 and determining if

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            capable of modulating the interaction of chemotactic chemokine (CCR5) with gp120, comprising incubating the against the agains
                                                                                                                                                                    human immuno deficiency virus; HIV; long terminal repeat; LTR, chemokine receptor; CKR; cellular dysfunction; HIV infection; CC-CKR-5; envelope glycoprotein: anti-urv
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10-JUL-2001.

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19-JUN-1996;
19-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contains a gene encoding CD4, a construct encoding a reporter gene under the regulation of an human immuno deficiency virus (HIV) long terminal repeat (LTR) and that has been transduced with a vector encoding a human chemokine receptor (CKR) where the CD4 and the CKR are present on the cell surface of transformed mammalian cell. The invention is useful for identifying drugs or antibodies that interfere with the translocation of HIV into transformed mammalian cell or for identifying a human chemokine receptor that facilitates the infection of a particular HIV strain into the transformed mammalian cell. Compounds identified can be used to treat cellular dysfunction and to prevent or combat HIV infection who recent companies the infection and to prevent or combat HIV infection who recent companies the infection and to prevent or combat HIV infection who recent companies the infection and to prevent or combat HIV infection who recent companies the infection and to prevent or combat HIV infection who recent companies the infection and to prevent or combat HIV infection who recent to the recent of the infection and to prevent or combat HIV infection who recent to the recent of the infection and the recent of the infection and the recent of the recent of the infection and the recent of the infection of the infection and the recent of the infection of the infection and the infection of the infection of the infection and the infection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                identified can be used to treat cellular dysfunction and to prevent or combat HIV infection. The present sequence is a human chemokine receptor (CKR), CC-CKR-5 related protein. CC-CKR-5 is the principal cofactor for entry mediated by the envelope glycoproteins of primary macrophage-tropic
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N-PSDB; AAD08577.
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Pred. No. 3.6e-200;
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18-JUN-2002

(first entry)

chemokine

0-0

motlf)

receptor 5 polypeptide

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The specification also describes an isolated polynucleotide comprising a nucleotide sequence which is a polynucrphic variant of the reference CCR5 gene sequence and comprises an isogene defined by a haplotype described in the specification and its encoded polypeptide. The methods of the claventh of the specification and its encoded polypeptide. The methods of the claventh of the specification of the gene. The CCR5 associated with abnormal expression or function of the gene. The CCR5 isogenes and the screened compounds are useful for treating human clammondeficiency virus (HIV)-1 infection and the progression to acquired immunodeficiency syndrome (AIDS). The invention has antiviral applications. The specification describes genotyping the CCR5 gene of an individual; predicting a haplotype pair for the CCR5 gene of an individual; identifying an association between a trait and a haplotype or CC individual; if the CCR5 gene. The specification describes a composition comprising a genotyping oligonucleotide for detecting a CCR5 polymorphism; a recombinant non-human organism transformed with CCR5 polymorphism; a recombinant non-human organism transformed with CCR5 colymorphism; a recombinant non-human organism transformed for the CCR5 colymorphism; a recombinant non-human organism transformed for detecting a CCR5 polymorphism; a recombinant non-human organism transformed for the CCR5 colymorphism; a recombinant non-human organism transformed for the CCR5 colymorphism; a recombinant non-human organism transformed for the CCR5 colympication detecting the CCR5 polympication and a method for screening drugs targeting the CCR5 polympication and a method for screening drugs targeting the CCR5 polympication and a method for screening drugs targeting the CCR5 polympication and a method for the CCR5 polympication and a metho
                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of a polypeptide encoded by the human chemokine (C-C motif) receptor 5 (CCR5) gene of the invention (see ABA97318, ABA97319). The specification describes haplotyping the CCR5 gene of an individual by determining if the individual has one of the CCR5 haplotypes or haplotype pairs fully defined in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Choi
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Sequence
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DB; ABA97318, AE
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352
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de polymorphism; SNP; human
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drug screening;
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MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60

Best Loc Matches

352;

Local

Similarity

100. Marity 100. Conservative

99

Score 1841; Pred. No. 3.6); Mismatches

DB 23; .6e-200;

0

Indels

0

Gaps

The invention relates to a method for identifying a binding compound for CC chemokine receptor 5 (CCR5). The method involves screening a library of test molecules (particularly peptides) with immobilised CC and then identifying those molecules which bind. The invention also relates to CCR5-binding molecules identified using the method of the invention, methods for identifying consensus motifs for CCR5-binding invention, methods for identifying consensus motifs for CCR5-binding

CCR5

Identifying CC chemokine receptor 5 binding compound for treating comprises binding a molecule from library to a molecule having bin property corresponding to CCR5 and identifying bound molecule -

Example

F1g

4A;

50pp; English.

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Query Match

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RESULT 10
AAM52828
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21-MAR-2000;
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DB; ABA02317.
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                                                                                                                                   Wilson
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2000US-191299P.
2001US-0813448.
2001US-0813651.
2001US-0813653.
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                                                                                                                                                                                                                                                                                        identification
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5
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                                                                                                                                                                                                                                                                                               eptor 5; human; HIV infection;
virus; AIDS; acquired immunodeficiency syndrome;
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                                                                                                                                   RH,
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N-PSDB; AAZ24738

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RESULT 11
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WPI;
                                                                                                                            21-OCT-1999
                                                                                                                                                     W09953033-A1
                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                               chemokine receptor; ss2 adrenergic receptor; small G-protein rho; renal outer medullary potassium ion channel protein; ion-channel lambda phage repressor protein; G-protein coupled receptor; bactebiochemical; vaccine; immunohistochemical; orphan receptor; HIV.
                                                                                                                                                                                                                                                                  Prostaglandin;
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                                                                                                   16-APR-1999;
                                                                                                                                                                              Homo sapiens.
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                                                 VANDERBILT
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                                                                                                                                                                                                                                                    PG; E2EP3 receptor; E2EP2 receptor; CCR-5; human; ptor; ss2 adrenergic receptor; small G-protein rho
                                                                          9805-0081989
                                                                                                                                                                                                                                                                                          containing
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                                                                                                                                                                                                                                                                                                                                                                    Protein;
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Pred. No. 3
                                                                                                                                                                                                                                                                                          chemokine receptor
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1.6e-200;
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В

Query Match

Length

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Local

Sequence

439

AA;

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The invention provides isolated nucleic acid sequences that encode rabbit CC prostaglandin (PG) E2EP3 receptor, human PG E2EP2 receptor, human CC chemokine receptor CCR-5, human ss2 adrenergic receptor, rat renal outer meduliary potassium ion channel protein or human small G-protein rho, CC together with deduced protein sequences. Also provided is a method for the production of eukaryotic proteins by culturing bacteria transformed CC with vectors containing the above nucleic acid sequences or a nucleic caid (I) that comprises: (i) first sequence that encodes either a comprising at least three positively charged amino acids, or a containing protein, or a lambda phage repressor protein, placed upstream CC of, and in frame with, (ii) a sequence encoding a protein. (I) are used CC proteins, G-protein coupled receptors or ion-channel proteins, in CC bacteria. These proteins are useful for blochemical or structural contingency as therapeutic agents; in diagnostic and screening assays and as antigens for use in vaccines, and for raising antibodies that are useful cas immunchistic chamical markers are for or the proteins.
                                        as immunohistochemical markers, e.g. for orphan receptors o
channels. Antibodies raised against the chemokine receptor
used (when administered as antiserum or generated in vivo)
entry of human immune deficiency virus (HIV) into cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 49-53; 81pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preventing HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic proteins in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acid constructs
bacteria, for pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  r producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for high level expression of eukaryotic roducing e.g. chemokine receptor CCR-5 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English
                                                                                                                           for orphan receptors or ion
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Best Loc
Matches
    379
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                                                                                                                                                                                                                                                                                                                              1 Similarity
352; Conserv
                                                                    MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV
                                                                                                                                                                                                                                     LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII
                                                                                                                                                                                                                                                                        HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI
                                                                                                                                                                                LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS
                                                                                                                                                                                                                     LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII
                            GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL
                                                       MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV
                                                                                                            HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI
                                                                                                                                                                LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS
                                                                                                                                                                                                                                                                                                                              100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                              Score 1841;
Pred. No. 4.8
0; Mismatches
                                                                                                                                                                                                                                                                                                                              1841; DB 20;
No. 4.8e-200;
smatches 0;
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CC chemokine receptor 5; CCR5; G-protein coupled receptor;
                            Human
                                         08-JUN-1998
                                                                 AAW23834
        immunodeficiency
                            S
                            chemokine
                                                                 standard;
                                        (first
                          receptor 5
                                                                  Protein;
                                      entry)
         virus;
                                                                  371
         HIV;
                            (CCR5)
                            A127V variant.
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                                                                                                                       Query Match
Best Local Similarity
Matches 351; Conser
                                                                                                                                                   from an isolated CDNA clone (see AAT76919). The conservative variation should not affect the activity of CCRS. The susceptibility of human macrophages to HIV infection depends on cell surface expression of CD4 and CCR5. CCRS is a member of the 7-transmembrane superfamily of 6-protein coupied cell surface molecules. It plays an essential role in the membrane fusion step of infection by some HIV isolates. The establishment of stable, non-human cell lines and transgenic mammals having cells that coexpress human CD4 and CCR5 provides valuable tools for research of HIV infection. Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding agents capable of blocking membrane fusion between HIV and target cells represent potential anti-HIV therapeutics for macrophage
                                                                                                                                                                                                                                                                                                                                                         fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Domain
                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                       Alkhatib G, Berger EA, Bro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                            tropic strains of HIV.
                                                                                                                                                                                                                                                                                     AAW23835) that has been designated CCR5.
                                                                                                                                                                                                                                                                                                           This protein sequence comprises an Alal27Leu variant of a novel
                                                                                                                                                                                                                                                                                                                                   Example 1; Fig 1B; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                       chemokine receptor 5 polypeptide sion between HIV and a target cell
           61
                               20
                                                                                                                                                                                                                                                                                                 macrophage-selective CC
LKSMTDIYLLNLAISDLFELLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFESGIFFII
                              MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR
                                                                                                                       371
                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0018508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label- III
/note- "transmembrane
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                                                                                    99.7%;
99.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Broder CC,
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                                                                        Score 1836; DB 19;
Pred. No. 1.4e-199;
D; Mismatches 1;
                                                                                                                                                                                                                                                                                                chemokine receptor (see also
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Combadiere
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                                                                                                                                                                                                                                                                                     The sequence was deduced
                                                                                                                                                                                                                                                                                                                                                                   င်
                                                                                                                                                                                                                                                                                                                                                                   inhibit membrane
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                                                                                                                                                                                                                                                             The susceptibility
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                            Query Match
Best Local Sim
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RESULT 13
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N-PSDB;
                                                                                                                                                                                                                                                           The invention relates to G protein-coupled receptors (GPCRs) for which the endogenous ligand has been identified. Non-endogenous constitutively activated versions of known GPCRs are used in the invention for the direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists. Such agonists are useful as therapeutic agents for diseases or disorders agonists are useful as therapeutic agents for diseases or disorders agonists are useful as therapeutic agents for diseases or disorders agonists are useful as therapeutic agents for diseases or disorders agonists are useful as therapeutic agents for diseases or disorders agonists are useful as therapeutic agents for diseases or disorders agonists are useful as therapeutic agents for diseases or disorders agonists are useful as therapeutic agents for diseases or disorders agonists are useful as therapeutic agents for diseases or disorders agonists are useful as therapeutic agents for diseases or disorders agonists agonists are useful as the disorders agonists agonists are useful as the disorders agonists are useful as the disorders agonists agonists agonists are useful as agonists 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying agonists of G protein-coupled receptors (GPCRs) for use disease treatment; comprises contacting candidate compounds with versions of GPCRs -
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constitutively activated GPCR; agonist; disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB56342;
                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 277-278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lehmann-Bruinsma K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-2001; 2001WO-US11098
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                                                                                                                                                                                                                                   version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AREN-) ARENA PHARM INC.
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DB; ABI97978.
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h 99.7%;
Similarity 99.7%;
51; Conservative
                                                                                                                                                                                                                                   of.
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                                                                                                                                                                                                                                   GPCR.
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Score 1835; DB 22;
Pred. No. 1.7e-199;
D; Mismatches 1;
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                                                               Length
                                                                           352;
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MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR

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Gaps

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RESULT 14
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ID AAM52
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20-MAR-2001;
20-MAR-2001;
20-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                      drug
 The for
                                             Identifying CC chemokine receptor 5 binding compound for treating AIDS, comprises binding a molecule from library to a molecule having binding property corresponding to CCR5 and identifying bound molecule
                                                                                                                                                                                           21-MAR-2000;
21-MAR-2000;
                                                                                                                                                                                                                                                                                       Misc-difference
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                             Example 3;
                                                                                      N-PSDB;
                                                                                                                Nestor
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 invention relates to CC chemokine receptor
                                                                                    2002-010610/01.
DB; ABA02318.
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                                                                                                                                                                                                                                                                                                                                                               CC chemokine receptor 5; human; HIV infection; immunodeficiency virus; AIDS; acquired immunodeficiency
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                                                                                                                JJ,
                                                                                                                                   CONSENSUS PHARM
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                           Fig 4B;
                                                                                                               Wilson
                                                                                                                                                    ; 2000US-190946P.
; 2000US-190996P.
; 2000US-191299P.
; 2001US-0813448.
; 2001US-0813651.
; 2001US-0813653.
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                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                       identification; variant.
                                                                                                                                                                                                                                                                             /note= "Encoded by AGC"
                                                                                                                                                                                                                                                                                                                                                                                            variant
                                                                                                                CJ,
                           50pp; English.
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method for 5 (CCR5).
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for*identifying a binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC library of test molecules (particularly peptides) with immobilised CCR5, cand then identifying those molecules which bind. The invention also crelates to CCR5-binding molecules identified using the method of the clivention, methods for identifying consensus motifs for CCR5-binding peptides, a transfer vector encoding tagged CGR5, a computer-aided methods for determining the relative binding affinity of a test molecule to CCR5 and a computer aided drug screening assay that utilises the cCR three-dimensional structure of CCR5. Compounds identified using the computer aided drug screening assay that utilises the cCR methods of the invention are useful for treating or preventing HIV CC (human immunodeficiency virus) infection or AIDS (acquired immunodeficiency syndrome) in a patient. The methods of the invention CC may also be used to identify agonists or antagonists of the interaction CC CCR5. The present sequence represents a naturally occurring variant of human CCR5 in which there is a glutamine, rather than a leucine, at
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       position 55.
                                                                 241
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                                                                                                                                                                                                               LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS
MIVYELFWAPYNIVLLLNTEQEEFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV
                                                                                                                                                                                                                                                            LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII
                                                                                                                                                                                                                                                                               LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII
                                                               HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI
                                                                                                                                 HFPYSQYQFWKNFQTLKIVILGLYLPLLYMVICYSGILKTLLRCRNEKKRHRAVRLIFTI
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                                                                                                                                                                                                                                                                                                                                                                                                        99.7%;
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                                                                                                                                                                                                                                                                                                                                                                                       Score 1835; DB 23;
Pred. No. 1.7e-199;
0; Mismatches 1;
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     352
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ARESULT 15
AREOTOR9
ID AREOT
XX AREOT
AC AREOT
AC AREOT
AC AREOT
XX 16-OC
XX 16-OC
XX Human
KW Human
KW Cytos
KW Ineuro
KW Ine
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#2

Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV; human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; cytostatic; immunosuppressive; nootropic; neuroprotective; gene therapy; neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia.

Homo sapiens

WO200158915-A2

09-FEB-2001; 2001WO-US04152.

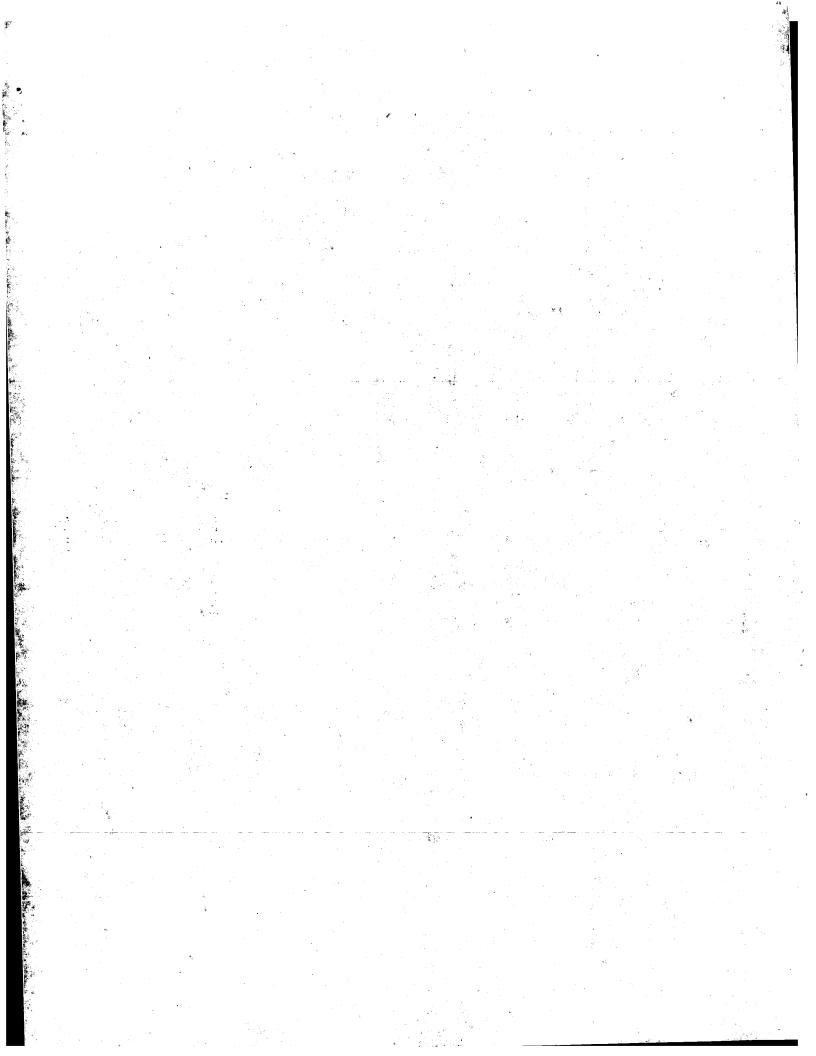
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                                                                                                                                                                                                                                                                                                                                                                                   pheumocytis carinii pneumonia or Raposi's sarcoma or defective or disordor may also be an infection disease (e.g. a viral infection such as an early stage HTV infection, a cytomegalovirus infection, or a serior and infection, an autoimmune disease (e.g. rheumatoid arthritis) or neurodegenerative disorder. The disease or disorder may be associated with aberrant CCR5 syrression, lack of CCR5 function. Aberrant CCR5 viral infection is used as a food additive or preservative to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA, protein, antibodies, agonists and antagonists are also useful in the disease, multiple sclerosis, rheumatoid arthritis and ulcerative consisting immune disorders (Addison's disease, multiple sclerosis, rheumatoid arthritis and ulcerative.
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Matches 351;
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Best Local :
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09-MAR-2000;
22-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid encoding a human G-protein chemokine receptor (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is human G-protein chemokine receptor (CCRS) HDGNR10 protein. CCRS HDGNR10 antibodies are useful for treating, preventing or ameliorating a disease or disorder associated with inflammation, defective or aberrant chemotaxis of immune cells, HIV infection (such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 40; Page 486-487; 495pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorders and neurodegenerative disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
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DB; AAD13198.
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GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
                                      HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI
                                                                                                                                                                                                            LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII
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; 2000US-0187999.
; 2000US-0234336.
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Pred. No. 2.9e-199;
0; Mismatches 1;
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301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTEEQEISVGL 352

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Search completed: June Job time: 66.5644 secs 3, 2003, 15:19:02



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Run on:
                                                                                             OM protein -
                                                                                        protein search, using sw model
                                              June 3,
                                                                                                                                                           GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
2003, 15:16:36; Search time 32.2822 Seconds (without alignments) 1048.235 Million cell updates/seb
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Title: Perfect score: Sequence: US-09-939-226-5 1841 1 MDYQVSSPIYDINY

MDYQVSSPIYDINYYTSEPC.....ERASSVYTRSTGEQEISVGL 352

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters:

283224

RESULT 1

Minimum Maximum DB seq length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Regult No.	Score	Query	Length	BG	IB	Description
1	1841	100.0	352	ນ	A43113	chemokine (C-C) re
N	1364	74.1	360	N	JC2443	(c-c)
w	1224	•	374	N	138450	(C-C)
•	1055	57.3	355	N	A45177	(0-0)
_C	1007.5	•	355	N	I49339	inflam
6	1001.5	•	359	N	I49341	MIP-1 alpha recept
7	935.5	•	355	N	G02436	C-C) r
8	919	•	360	N	A57160	(c-c)
9	906	•	360	N	JC4587	(0-0)
10	829	45.0	383	ผ	S55594	G protein-coupled
11	799.5	٠	356	ผ	I49340	MIP-1 alpha recept
12	746.5	•	355	ผ	JC5067	G protein-coupled
13	712	•	354	N	158186	probable G protein
14	-	•	344	N	JC5942	chemokine receptor
15	670.5	٠	355	N	JC4304	orphan G protein-c
16	567	٠	378	ผ	B55735	lymphocyte-specifi
17	562	•	378	N	A55735	G protein-coupled
18	559		369	ผ	JC5068	G protein-coupled
19	553	•	378	ผ	A45680	G protein-coupled
20	541	•	333	ผ	165989	G protein-coupled
21	521	•	360	N	A53611	interleukin-8 rece
22	517.5	•	359	N	A48921	interleukin-8 rece
23	515	•	355	N	JQ1231	interleukin-8 rece
24	514.5	•	358	ผ	A53752	interleukin-8 rece
25	510.5	27.7	367	N	JE0349	interferon-inducib
26	509.5	•	350	N	JN0621	G protein-coupled
27	506.5	•	350	ผ	A39445	interleukin-8 rece
28	506	•	352	N	G00048	fusin (LESTRA) - c
29	506	27.5	352	ພ	A45747	neuropeptide Y/pep

A;Accession: Tree mana A;Accession: Type: mana A;Accession: Type: mana A;Residues: 1-352 <COMI>
A;Residues: 1-352 <COMI>
A;Cross-references: GB:U57840; NID:g1502408; PIDN:AAB17071.1; PID:g1502409
A;Cross-references: GB:U57840; NID:g1502408; PIDN:AAB17071.1; PID:g1502409
A;Cross-references: GB:U57840; NID:g1502408; PIDN:AAB17071.1; PID:g1502409

J. Leukoc. Biol. 60, 147-152, 1996
A;Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine A;Reference number: A58832; MUID:96295970; PMID:8699119

R;Combadiere, C.
submitted to the EMBL Data Library, May 1996
A;Reference number: H01541
A;Accession: G02653

A; Status: translated from GB/EMBL/DDBJ

A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rosldues: 1-89,'L',91-352 <COM2>
A;Residues: 1-89,'L',91-352 <COM2>
A;Residues: 1-89,'L',91-352 <COM2>
A;Residues: 1-89,'L',91-352 <COM2>
A;Cross-references: EMBL:U57840

J; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
J. Biol. Chem. 271, 17161-17166, 1996
A;Title: Molecular cloning and functional characterization of a novel human CC chemok
A;Reference number: A58833; MUID:96291862; PMID:8663314

45	44	٠ پ	42	41	40	39	38	37	36	35	34	33	ພ	31	30
453	460.5	461	461	461.5	464.5	466.5	468.5	468.5	469.5	471	472	473.5	474.5	490.5	496.5
24.6	25.0	25.0	25.0	25.1	25.2	25.3	25.4	25.4	25.5	25.6	25.6	25.7	25.8	26.6	27.0
374	359	372	327	359	359	359	359	359	359	359	374	359	359	356	353
N	N	ພ	N	N	N	N	N	N	N	N	N	N	N	ຎ	Ν
S32785	A48857	S26667	S56162	JC1104	JQ1516	S15403	JC1194	S44425	JH0621	151372	S42628	A42656	JC2134	S42096	S28787
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G protein-coupled	angiotensin II rec	G protein-coupled	MDCR15 protein -	angiotensin II rec	anglotensin II rec	angiotensin II rec	angiotensin II rec	anglotensin II rec	angiotensin II rec	angiotensin II rec	G protein-coupled	angiotensin II rec	angiotensin II rec	interleukin-8 rece	neuropeptide Y/pep

ALIGNMENTS

J. Leukoc. Biol. 60, 147-152, 1996 J. Leukoc. Biol. 60, 147-152, 1996 A;Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine A;Reference number: A58832: MUID:96295970: PMID:8699119	A;Note: this frameshift mutation results in a non-functional receptor but confers a d nod may have had a selective advantage by confering resistance to Yersinia plague inf	A;Residues: 1-184,'IKDSHLGAGPAAACHGHLLLGNPKNSASVSK' <sam3> A;Cross-references: GB:X99393; NID:g1524062; PIDN:CAA67767.1; PID:g1524063</sam3>	A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: DNA	¿ A;Residues: 182-206;207-230 <sam2> A;Accession: A58834</sam2>	A;Status: nucleic acid sequence not shown; not compared with conceptual translation.	A;Accession: S71808	A; Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant aligie A; Reference number: S71808; MUID:96345670; PMID:8751444	Nature 382, 722-725, 1996	M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.;	R; Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saraq	A:Cross-references; GB:X91492: NID:q1262810: PIDN:CAA62796.1: PID:q1262811	A: Molecule type: mRNA	A; Accession: A43113	A; Title: Molecular cloning and functional expression of a new human CC-chemokine rece	Biochemistry 35, 3362-3367, 1996	R;Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.	C;Accession: A43113; S71808; A58834; A58832; G02653; A58833	C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 20-Jun-2000	C; Species: Homo sapiens (man)	N;Alternate names: C-C CKR-5; CCR5	chemokine (C-C) receptor 5 - human	A43113 = A43113

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C;Accession: U.T. Crimer, T. Crimer, C;Amagami, S; Tokuda, Y; Ishir, T. 156-1162, Iss. Biochem. Biophys. Res. Commun. 202, 1156-1162, Iss. Biophys. Res. Commun. 202, Iss. Biophys. Res. Biophys. Res. Biophys. Res. Biophys. Res. Biophys. Res. Biophys. Biophys. Res. Biophys. Biophy
                                                                                                                                                                                                                                                                                                                                          C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 C;Accession: JC2443; I38463
                                                                                                                                                                                                                                                                                                                                                                                                           N; Alternate
C; Species: 1
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F;268/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map posit
C; Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A58833
A; Molecule type: mRNA
A; Residues: 1-352 <RAP>
                 A;MClecule type: mRNA
A;Mclecule type: mRNA
A;Residues: 1-360 <YAM>
A;Cross-references: DDBJ:D29984; NID:g531246; PIDN:BAA06253.1; PID:g531247
A;Cross-references: DDBJ:D29984; NID:g531246; PIDN:BAA06253.1; PID:g531247
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                                                                                                                                                                                                                                                                                                                                                                                                        Species: Homo sapiens (man)
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (C-C) receptor 2,
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Myers, S.J.; Herman, A.; Fran
ad. Sci. U.S.A. 91, 2752-2756,
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OMIM:601373
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A; Map position: 3p21-3p21
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate splicing; G protein-coupled rec
C; Keywords: alternative splicing; G protein-coupled rec
F; 43-70/Domain: transmembrane #status predicted <TM2>
F; 81-100/Domain: transmembrane #status predicted <TM2>
F; 115-136/Domain: transmembrane #status predicted <TM4:
F; 154-178/Domain: transmembrane #status predicted <TM4:
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A; Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;207-226/Domain: transmembrane #status predicted <TM5>F;244-268/Domain: transmembrane #status predicted <TM6>F;244-268/Domain: transmembrane #status predicted <TM7>F;287-309/Domain: transmembrane #status predicted <TM7>F;14/Binding site: carbohydrate (Asn) (covalent) #status F;113-190/Disulfide bonds: #status predicted
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C; Genetics:
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                     VFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL
                                                                       PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS
                                                                                             PYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL
                                                                                                                                                   WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT
                                                                                                                                                                                     WKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWA
                                                                                                                                                                                                                             IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----
                                                                                                                                                                                                                                                                                                                             LNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLA
                                                                                                                                                                                                                                                                                                                                                                                 FDYDY---GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL
VFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL
                                                                                                                                                                                                                                                                                                       LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDB:337364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL:U03905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74.18;
75.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NID:g472557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1364;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein-coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1es 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIDN: AAA19120.1;
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                                     352
360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PID:g472558
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                                                                         317
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                                                                                                                                                                                                                                                                                                     141
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                                                                                                             309
                                                                                                                                                   257
                                                                                                                                                                                                                             197
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RESULT 138450

Species: Homo sapiens (man)

or 2, splice form CKR-2; monocyte o

monocyte

16-Feb-1996

#text_change 13-Aug-1999

S

1 A - human chemoattractant protein 1 receptor; monocyte

N;Alternate names: C-C CKR C;Species: Homo sapiens (ma C;Date: 16-Feb-1996 #sequen C;Accession: T22/F A; Gene: GDB: CMKBR2
A; Cross-references: (
A; Map position: 3p21:
C; Superfamily: vertel A;Molecule type: mRNA A;Residues: 1-374 <RES> A;Cross-references: EMBL:U03882; NID:g472555; A;Title: Molecular cloning and functional expression of A;Reference number: A53477; MUID:94195821; PMID:8146186 A;Accession: I38450 A; Cross-references: C; Genetics: R;Charo, I.F.; Myers, S.J.; Herman, Proc. Natl. Acad. Sci. U.S.A. 91, 27 Date: 16-Feb-1996 #sequence_revision Accession: 138450 Status: preliminary 3p21-3p2 GDB:337364; OMIM:601267 n, A.; Franci, C.; 2752-2756, 1994 PIDN: AAA19119.1; Connolly, t WO monocyte chemoattractant А.Л.; PID:g472556 Coughlin,

transmembra

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C;Keywords: alternative splicing; G protein-coupled receptor, yajoo F;44-68/Domain: transmembrane #status predicted <TM1> F;74-99/Domain: transmembrane #status predicted <TM2> F;115-136/Domain: transmembrane #status predicted <TM3> F;1154-178/Domain: transmembrane #status predicted <TM4> F;154-178/Domain: transmembrane #status predicted <TM4> F;208-226/Domain: transmembrane #status predicted <TM5> F;248-265/Domain: transmembrane #status predicted <TM5> F;244-265/Domain: transmembrane #status predicted <TM7> F;147Binding site: carbohydrate (Asn) (covalent) #status predicted F;33-277,113-190/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
A45177
chemokine
                                                                                                                                                                                                                                                                                                                                                                                                   chemokine (C-C) receptor 1 - human N;Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor C;Species: Homo ampiens (man) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999 C;Accession: A45177; I55671 R;Necte, K:; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J. Cell 72, 415-425, 1993 A;Title: Molecular cloning, functional expression, and signaling characteristic A;Reference number: A45177; MUID:93161416; PMID:7679328
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                 A;Gene: GDB:CMKBR1; CMKR-1
A;Crose: references: GDB:138446; OMIM:601159
A;Map position: 3p21-5p21
C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                              A;Reference number: I55671; MUID:93240122; PMID:7683036
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                                                                                          A;Cross-references:
C;Genetics:
                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-355 <RES>
                                                                                                                                                                                                                 R;Gao, J.
J. Exp. Med. 177, 1421-1427, 1993
A;Title: Structure and functional
                                                                                                                                                                                                                                                                          A;Rosiduos: 1-355 <NEO>
A;Rosiduos: 1-355 <NEO>
A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1;
A;Experimental source: HL60 cells
A;Note: sequence extracted from NCBI backbone (NCBIP:124876)
                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                    A; Status: nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A45177
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Best Local Similarity 76.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEFQKHIA 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----RG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AIH----
lfide bond; G
                                                                                                             GB:L10918; NID:g292416; PIDN:AAA36543.1;
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protein-coupled
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                                                                                                                                                                                                                                                                                                                                                                      not shown
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Pred. No. 8.2e-94;
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receptor;
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glycoprotein; phosphoprotein;
                                                                                                             PID: g292417
                                                                                                                                                                                                                                                                                                                PID:g292417
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macrophage inflammatory protein-1 alpha receptor - mouse C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_char C;Accession: I49339
R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression A;Reference number: I49339; MUID:95340546; PMID:7542241
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F;288-305/Domain: transmembrane #status predicted <TM7>
F;5/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;24-273,106-183/Disulfide bonds: #status predicted
F;345/Binding site: phosphare (car) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-355 <RES>
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F;147-171/Domain: transmembrane #status predicted <TM4>
F;205-223/Domain: transmembrane #status predicted <TM5>
                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:U28404; NID:g881547; PIDN:AAA89153.1; PID:g881548 C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A; Accession: I49339
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                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                              Local Similarity
les 190; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126
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197; Conserv
                                                                                            75
                                                                                                                                       71
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                                                                                                                                                                                                                          11 DINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                            VVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFPYSQYQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.3%; Score 1055; DB 2; ilarity 56.1%; Pred. No. 7.4e-80; Conservative 59; Mismatches 89;
                                                                                                                                                                                                                                                                         54.7%;
llarity 55.6%;
Conservative 5
                                                                                                                                                                                                                                                                              55;
                                                                                                                                                                                                                                                                         Score 1007.5; DB 2;
Pred. No. 6.2e-76;
5; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             from GB/EMBL/DDBJ
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RESULT 7
G02436
chemokine
                                                                                      N;Alternate names: C-C CKR-3
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision
C;Accession: G02436; A57237
R;Ponath, P.D.
                                                           submitted to the EMBL Data Library, A; Reference number: H01272
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J. Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression A;Reference number: 149339; MUID:95340546; PMID:7542241
A;Accession: 149341
   A; Molecule type: DNA
A; Residues: 1-355 < PO
                                          A; Reference number: A; Accession: G02436
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;Species: Mus musculus (house mouse)
;Date: 02-Jul-1996 #sequence_revision
                              Status: translated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: vertebrate
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                                                                                                                                                                                                                                                                   QKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISV 350
                                                                                                                                                                                                                                                                                                LVLLFSAFHSTFLETSCEQSKHLDLAMQVTEVIAYTHCCVNPVIYAFVGERFRKHLRLFF
                                                                                                                                                                                                                                                                                                                 IVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLLVFF
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Pred. No. 2e-75;
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A;Cross-references: GB:X85740;
A;Note: source clone K5-5
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RESULT 8
A57160
A57160
A57160
A57160
Chemokine (C-C) receptor 4 - human
N;Alternate names: C-C CKR-4
C:Species: Homo sapiens (man)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_cl
C;Accession: A57160
R;Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewel
J. Biol. Chem. 270, 19495-19500, 1995
A;Title: Molecular cloning and functional expression of a R;Reference number: A57160; MUID:95370289; PMID:7642634
A;Accession: A57160
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C;Superfamily: vertebrate rhodopsin
C;Reywords: G protein-coupled receptor; glycoprotein; phosi
F;36-60/Domain: transmembrane #status predicted <TM1>
F;71-91/Domain: transmembrane #status predicted <TM2>
F;108-129/Domain: transmembrane #status predicted <TM3>
F;108-129/Domain: transmembrane #status predicted <TM4>
F;205-223/Domain: transmembrane #status predicted <TM5>
F;205-223/Domain: transmembrane #status predicted <TM6>
F;205-223/Domain: transmembrane #status predicted <TM6>
F;205-203/Domain: trans
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A; Residues: 1-106,'N'.108-275,'S',277-280,'R',282-355 <COM>
A; Residues: B: U28694; NID: g1199579; PIDN: AAC50469.1;
A; Note: the translated sequence in GenBank entry HSU28694, rel C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:U49727; NID:g1477560; PIDN:AAB09726.1; I R;Combadiere, C.; Ahuja, S.K.; Murphy, P.M.
J. Biol. Chem. 270, 16491-16494, 1995
A;Title: Cloning and functional expression of a human eosinophil A;Reference number: A57237; MUID:95348056; PMID:7622448
A; Status: preliminary; not A; Molecule type: mRNA
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A; Cross-references:
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A; Status: nucleic a
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Pred. No. 5.6e-70;
3; Mismatches 90
                                      conceptual translation
                                                                                                                                                                                                                        K.B.; Hoogewerf, A.J.; Proudfoot,
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NID: g1370103;

PIDN:CAA59743.1; PID:g971452

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RESULT 9
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A:Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to A:Roccession: JC4587; MUID:96138324; PMID:8573157
A:Roccession: JC4587
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A:Roferences: EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g1167852
A:Residues: 1-360 <HOO>
A:Residues: 1-360 <HOO>
A:Cro88-references: EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g1167852
A:Experimental source: thymus
C:Genetics:
A:Genetics:
A:Genetics: glycoprotein; phosphaprotein; receptor; thymus
C:Keywords: glycoprotein; phosphaprotein; receptor; thymus
C:A:Royards: glycoprotein; phosphate (Ser) (covalent) (by casein kinase I) #status predicted
F:72,702,350/Binding site: carbohydrate (Ser) (covalent) (by protein kinase C) #status predicted
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
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A:Gene: GDB:CMKBR4
A:Gene: GDB:CMKBR4
A:Cross-references: GDB:677463
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:KGywords: G protein-coupled recepto
F:40-65/Domain: transmembrane #status
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A; Molecule type: DNA
A; Residues: 1-383 <TEL>
A; Cross-references: GB:U20824; NID:g695172;
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: S55594
R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.;
J. Mol. Biol. 249, 520-528, 1995
A;Title: The DNA sequence of equine herpesvirus 2.
A;Reference number: S55594; MUID:93302501; PMID:7783207
A;Accession: S55594
A;Status: preliminary; nucleic acid sequence not shown
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;Species: equine herpesvirus 2
;Date: 10-Apr-1996 #sequence_revision
                                                                                                                NLAISDLEFLLTVPFWAHYAAA--QWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYL 128
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LVFFQKHIAKRFCKCCSIFQ----QEAPER
                                                APYNIVLLLNTEQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYL
                                                                                               AVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFPYSQYQ
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                             TPYNIVLLLSTFHATLLNLQCALSSNLDMALLITKTVAYTHCCINPVIYAFVGEKFRRHL
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Pred. No. 3.9e
64; Mismatches
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C;Accession: I49340
C;Accession: I49340
R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression
A;Title: Cloning and differential tissue-specific expression
A;Title: Cloning and differential tissue-specific expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: 149339; MUID:95340546; PMID:754
A;Accession: 149340
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                          G protein-coupled receptor CKR-L1 - human
N;Alternate names: chemokine receptor-like protein TER1; GPR-CY6
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C;Accession: JC5067; G02776; G02387
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A; Residues: 1-356 < RES>
                                                                                                                                                          R;Napolitano, M.; Zingoni, A.; Berna
submitted to the EMBL Data Library,
A;Reference number: H01714
                                                                                                                                                                                    A;Cross-references: EMBL:279782; NID:g1668735; R;Napolitano, M.; Zingoni, A.; Bernardini, G.; submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                      R;Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G
Blochem. Blophys. Res. Commun. 227, 846-853, 1996
A;Title: Molecular cloning and RNA expression of two new human
A;Reference number: JC5067; MUID:97040707; PMID:8886020
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A; Residues: 1-355 < ZAB>
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                                                                                         A; Molecule type: DNA
                                                                                                                   A;Status:
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Best Local
                                        Cross-references: EMBL:U62556; NID:g1468978; PID:g1468979
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the EMBL
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Data Library,
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                                                                                                                   GB/EMBL/DDBJ
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Pred. No. 9.
January 1996
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Spinetti, G.; Ro
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RESULT 13
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A; Accession: G02387
A; Status: preliminar
                                                                                                                                                                                             Neurosci. Lett. 169, by Neurosci. Lett. 169, by A; Title: cDNA cloning of a G
                                                                                                                                                                                                                                                 probable G protein-coupled receptor - rat C;Species: Rattus norwegicus (Norway rat) C;Date: 26-Jul-1996 #sequence_revision 26 C;Accession: I58186 R;Harrison, J.K.; Barber, C.M.; Lynch, K.
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C; Keywords: G protein-coupled recep
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A; Cross-references: GDB: 6053
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C;Genetics:
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A; Residues: 1-354 < RES>
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                                                                                                                                                                                A; Accession: I58186
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73-94/Domain: transmembrane #status predicted <TM2>
108-130/Domain: transmembrane #status predicted <TM2>
                   Best
                                                                     Superfamily: vertebrate rhodopsin 
Keywords: G protein-coupled recep
                                                                                                                                                               Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 VYCKKLRSITDYYLLNLALSDLLFVFSFPFQTYYLLDQWVFGTVMCKVVSGFYYIGFYSS
147; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-355 <BON>
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                                                                                                         EMBL: U04808; NID: g2558635; PIDN: AAB87093.1;
                                                                                                                                                                                                   a G-protein-coupled
86; MUID:94323113; PA
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 59;
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OMIM:601834
Score 712; DB
Pred. No. 1.7e
59; Mismatches
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Pred. No. 2.4
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                   DB 2;
.7e-51;
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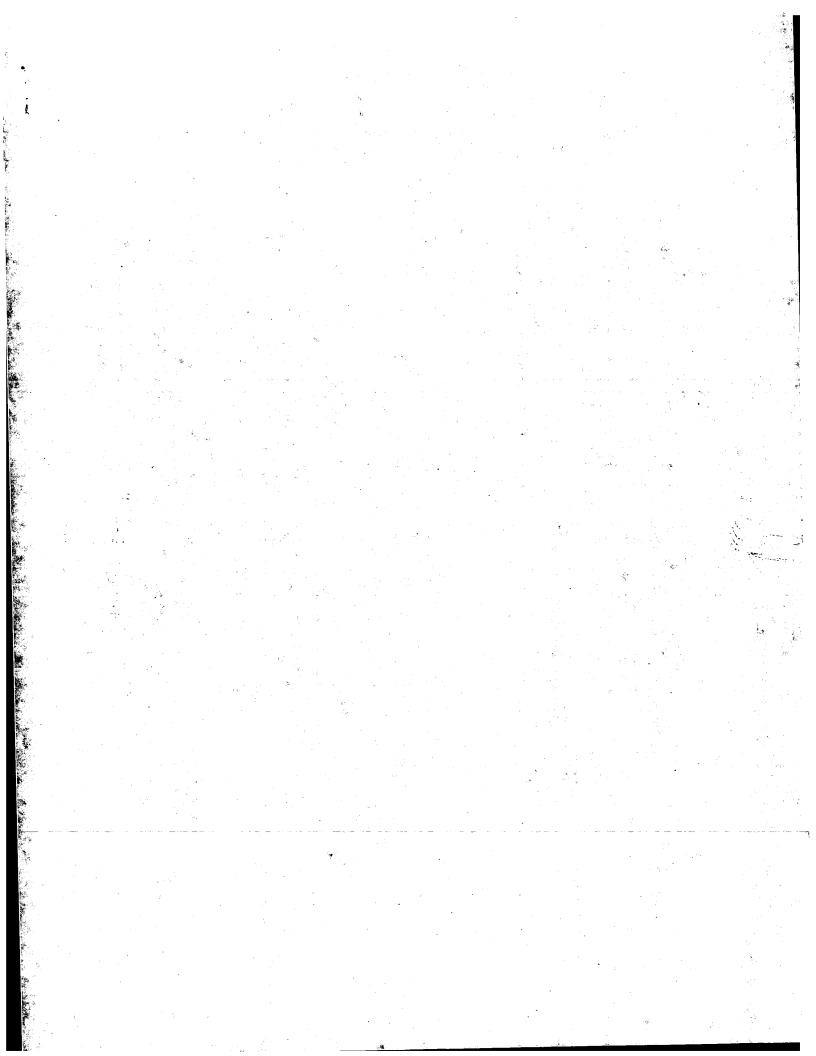
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RyFan, P.; Kybw, H.; Su, K.; Zong, Z.; Augustus, M.; Carter, K.C.; L1, Y. Blochem. Blophys. Res. Commun. 243, 264-268, 1998
A:Title: Cloning and characterization of a novel human chemokine receptor. A:Reference number: JC5942; MUID:98139902; PMID:9473515
A;Accossion: JC5942
A;Status: proliminary
A;Status: proliminary
A;Molecule type: DNA
A;Residues: 1-344 <FRN>
A;Cross-references: GB:U97123; NID:g2897070; PIDN:AAC39595.1; PID:g2897071
C;Superfamily: vertebrate rhodopsin
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chemokine receptor - human
C;Species: Homo sapiens (ma
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                            QKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQE 347
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                                                                                                                                                                                FSARRRYPCGIITSVLAWVTAILATLPEYVVYKPQMEDQKYKCAFSRTPFLPADETFWKH
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                                                                                     IVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLLVFF 312
                                                                                                                     FLTLKMNISVLVLPLFIFTFLYVQMRKTL---RFREQRYSLFKLVFAIMVVFLLMWAPYN
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                                                         IAFFLSTFKEHFSLSDCKSSYNLDKSVHITKLIATTHCCINPLLYAFLDGTFSKYL----
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illarity 40.9%;
Conservative 6/
CRCFIIL-RSNTPLQPRGQSAQGTSREE
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; Pred. No. 2.8e-48;
64; Mismatches 108;
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Search completed: June Job time : 34.2822 secs

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15:22:40

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A; Gene: A; A; Map position: 3pter-p21
A; Map position: 3pter-p21
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; lymphokine; transmembrane 5; 35-57/Domain: transmembrane 5 status predicted (TM2)
F; 166-88/Domain: transmembrane 5 status predicted (TM3)
F; 104-125/Domain: transmembrane 5 status predicted (TM4)
F; 146-165/Domain: transmembrane 5 status predicted (TM4)
F; 197-217/Domain: transmembrane 5 status predicted (TM5)
F; 197-254/Domain: transmembrane 5 status predicted (TM7)
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A; Residues: 1-355 < RAP>
A; Residues: 1-355 < RAP>
A; Cross-references: GB: U20350; NID: g665580; PIDN: AAA91783.1; PID: g665581
A; Experimental source: peripheral blood mononuclear cell
C; Comment: This protein is a cell-surface receptor which recognizes extracellular sig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           orphan G protein-coupled receptor - human
N;Alternate names: V28 protein
C;Species: Homo sapiens (man)
C;Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 19-May-2000
C;Accession: JC4304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: The orphan G-protein-coupled receptor-encoding A; Reference number: JC4304; MUID: 96011651; PMID: 7590284 A; Accession: JC4304
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Gene 163, 295-299,
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                                                                            LETLKLYDFFPSCDMRKDLRLALSVTETVAFSHCCLNPLIYAFAGEKFRRYLYHLYGKCL
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ilarity 42.98;
Conservative 55
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Pred. No. 4.6e-48;
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: June 3, 2003, 15:09:40 ; Search time 16.1411 Seconds (without alignments) 904.503 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-939-226-5 1841 1 MDYQVSSPIYDINYYTSEPC.....ERASSYYTRSTGEQEISVGL 352

Scoring table: BLOSUM62 Gapop 10.0., Gapext 0.5

Scarched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Prod. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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J. Virol. 71:8642-8656(1997).	s in infections	POLYMORPHISMS in the CCR5 genes of Airican green monkeys and mice	uhmann S.E., Platt E.J., Kozak S.L., Kabat	MEDLINE=98001387; PubMed=9343222;	SEQUENCE FROM N.A.	[5]	Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases	Watanahy A.M., Destiva C., Ciar-refer S., Endi A., Id I.,	COltrade V a Doctive T Distribution o story V V: V	POTTO-1 B M. DITATAN V. GARGACA, FILEGERALD M., See L.H., Young M.,			W.K., Wilson K., Chen E., Gibbs R., Zuo L., J	UENCE FROM N.A.		J. Leukoc. Biol. 60:147-152(1996).	RANTES.":	ň	Combadiere C., Ahuja S.K., Tiffany H.L., Murphy P.M.;	MEDLINE=96295970; PubMed=8699119;	SEQUENCE FROM N.A.	J. Biol. Chem. 271:17161-17166(1996).	CC chemokine receptor (CCR5) for RANTES, MIP-lbeta, and MIP-lalpha.*;	"Molecular cloning and functional characterization of a novel human	Raport C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F.;	MEDLINE=96291862; PubMed=8663314;	SECTION FROM N. P.	Biochemistry 35:3362-3367(1996).		l expression of a new human	, Vassart		CACHEROS AND A CACHERON AND A CACHER		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Chordata: Craniata: Vertebrata:	CCRO OR CHARDRO.		C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5)	15-JUN-2002 (Rel. 41, Last annotation update)	01-001-1996 (Rel. 34, Created)		014701; 014702; 014703; 014704; 014705; 014706;	014692; 014693; 014695; 014696;	S HUMAN . S	

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SEQUENCE FROM N.A., AND POLYMORPHISMS.
MEDLINE-98022612; PubMed-9359654;
Zhang L., Carruthers C.D., He T., Huar
  EMBL;
                         EMBL;
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"HIV-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHARACTERIZATION OF ITS HIV-1 R
MEDLINE-96260018; PubMed-864951
Dragic T. Litwin V. Allaway G
Nagashima K.A., Cayanan C., Mad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Identification of a major HIV-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARACTERIZATION OF ITS HIV-1 MEDLINE-96260017; PubMed-86495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND VARIANT ARG-178
Magierowska M., Barre-Sinoussi F., Issa
                                                  EMBL;
                                                                                     entities requires
                                                                                                                                                                                                                                                                                                                                                                                                       SULFATION.
                                                                                                                                                                                                                                                                                                                                                                                                                             Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 381:661-666(1996).
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                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99189752; PubMed=10089882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Debre
                                                                          send
                                                                                                                                                                      SUBCELLULAR LOCATION: Integral membrane protein. TISSUE SPECIFICITY: FOUND IN PROMYELOCYTIC CELLS. PTM: SULFATION CONTRIBUTES TO THE EFFICIENCY OF H PTM: MODIFIED BY O-LINKED GLYCOSYLATION, BUT NOT GLYCOSYLATION.

SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUP
                                                                                                                                                                                                                                         FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR DIFFERENTIATION. ACTS AS CO-RECEPTOR WITH CD4 FOR PRIMARY NON-SYNCYTIUM-INDUCING STRAINS (NSI) (MACROPHAGE-TROPIC) OF HIV-1 VIRUS. IT PROMOTES ENV-MEDIATED FUSION OF THE VIRUS.
                                                                                                                        European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Η.,
                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration entry is copyright. It is produced through a collaboration the Swiss Institute of Bioinformatics and the EMBL outstation.
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  U57840;
U95626;
U83326;
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                                       U54994;
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o P., Marmon S., Sutton R.E., H
.C., Schall T.J., Littman D.R.,
                                                                                                 non-profit institutions as long and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hum.
                                                                          email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subtypes, coreceptor usage, and CCR5 polymorphism.";
um. Retroviruses 13:1357-1366(1997).
                                                                                      this statement uires a license
  AAC50598.1;
AAB17071.1;
AAB57793.1;
AAC51797.1;
                                                  CAA62796.1;
                                                                                                                                                                       BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             co-receptor for primary isolates of
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                                                                                        agreement
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Hill C.M., Davis C.B.,
R., Landau N.R.;
                                                                                     (See http://www.isb-sib.
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                                                                                                                        There are no
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ITE; PS00237; G_PROTEIN_RECEP_F1_1; PS00237; G_PROTEIN_RECEP_F1_2; PS50262; G_PROTEIN_RECEP_F1_2;
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601373; -.
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AF011501;
AF011502;
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SULFATION:

Y -> D (IN INCCR5-71A).

/FIId=VAR_003481.

A -> S (IN DBSNP:1800939).

/FIId=VAR_011839.

R -> H (IN INCCR5-72A).
                                                                                                                                                            3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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CYTOPLASMIC (I
2 (POTENTIAL).
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                                                                                                                                        6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL)
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DT 15-JUL
DT 16-OCT
DE C-C ch
GN CCRS 0
OOS Pan tr
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Best Local
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CKR5_PANTR STANDAKU;
P56440; 002778;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
16-CCT-2001 (Rel. 40, Last annotation update)
                                                                          "Sequence
HIV type 1
                                                                                                                                                                                                                                                                                                                                                           MEDILINE-97268687; PubMed-9108095;
Edinger A.L., Amedee A., Miller K., Doranz B.J., End
Sharron M., Samson M., Lu Z.H., Clements J.E., Murph
Pelper S.C., Parmentier M., Broder C.C., Doms R.W.;
"Differential utilization of CCR5 by macrophage and
simian immunodeficiency virus strains.";
Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
                                                                                                                                                                                             Zhang
Ho D.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-97268687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pan troglodytes (Chimpanzee).
Eukaryota; Motazoa; Chordata;
Mammalla; Eutheria; Primates;
       SEQUENCE FROM N.A. MEDLINE-98090115;
                                                                                                     Zacharova V.,
                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-98022612;
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                                                                                                                      MEDLINE-97426118;
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                                                                      of chemokine
1 host.";
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                                                      Retroviruses
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har V., Goustin
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ers C.D., He T.,
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Pred. No. 9.6e-92;
; Mismatches 0;
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                                                                                     CCR5 in chimpanzees,
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E., Murphey-Corb
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-I- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-BETA AND RATTES AND SUBSEQUENTLY TRANSDUCES A S INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION
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PR00237; GPCRRHODOPSN.

PS00237; G_PROTEIN_RE

PS50262; G_PROTEIN_RE
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Eukaryota; Metazoa; Chordata;
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-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE.
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European Bioinformatics Institute
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16-OCT-2001
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Mammalia;
                          InterPro; IPR000276; or pfam; PF00001; 7tm_1;
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Eutheria;
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                                              GPCR_Rhodpsn.
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"Differential ULLIZACION OF GRANULOCYTIC LINEAGE PROLIFERATION OR
                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s
                                                                                                                                                                                                                                                                                            Eddinger A.L., Amedee A., Miller K., Doranz B.J., Endres M., Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey Corb Peiper S.C., Parmentier M., Broder C.C., Doms R.W.; "Differential utilization of CCR5 by macrophage and T cell t
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=97268687; PubMed=9108095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gorilla gorilla gorilla (Lowland gorilla)
                                                                                                                                                      SUBCELLULAR LOCATION: Integral membrane SIMILARITY: BELONGS TO FAMILY 1 OF G-PRO
AF005659; AAB62553.1;
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                             license agreement (S license@isb-sib.ch).
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Catarrhini;
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                                               (See http://www.isb-sib.ch/announce/
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Mammalia; Eutheria;
Trachypithecus.
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SEQUENCE FROM N.A.
MEDLINE-99416438; PubMed-10486970;
Zhang Y.-W., Ryder O.A., Zhang Y.-
"Sequence evolution of the CCR5 ch
                                                 Trachypithecus phayrei (Phayre's leaf monkey).
Eukaryota; Metazoa; Chordata; Craniata; Verteb
Mammalia; Eutheria; Primates; Catarrhini; Corc
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EXTRACELLULAR (POTENTIAL).

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EXTRACELLULAR (POTENTIAL).

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5 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

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CYTOPLASMIC (POTENTIAL).

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SULPATION (BY SIMILARITY).

SULPATION (BY SIMILARITY).
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Pred. No. 6.8e-91;
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nilarity 98.0%;
Conservative
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MO1. Biol. Evol. 16:1145-1154(1999).

-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1 MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
                                                                                                                                                                          DIFFERENTIATION.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                  ween the Swiss Institute of Bioinformatics Institute.
                          SWISS-PROT entry is copyright. It is produced through a collable een the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in fied and this statement is not removed. Usage by and for con
(See http://www.isb-sib.
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SULFATION (BY SIMILA
SULFATION (BY SIMILA Y SIMILARITY)
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N5938F CRC64; Sulfation

.1e-90; DB 1;

Length Indels

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Gaps

60

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240

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RESULT
CKR5_PI
  Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M., Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb Peiper S.C., Parmentier M., Broder C.C., Doms R.W.; "Differential utilization of CCR5 by macrophage and T cell t simian immunodeficiency virus strains."; Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
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PRINTS; PRO0237; GPCKRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_Fl_2; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_Fl_2; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_Fl_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein DOMAIN 1 30 EXTRACELLULAR (POTENTIAL)

TRANSMEM 31 58 1 (POTENTIAL).

TRANSMEM 59 68 CYTOPLASMIC (POTENTIAL).

TRANSMEM 69 89 2 (POTENTIAL).

TRANSMEM 69 89 2 (POTENTIAL).
                                                                                                                                                                       EMBL;
                                                                                                                                                                                                  EMBL; AF005658; AAB62552.1; -. EMBL; AF105287; AAD20556.1; -. EMBL; AF105288; AAD20557.1; -.
                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                              Benton P.A., Timanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-I-FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES-P.hamadryas;
MEDLINE-99210133; PubMed-10195758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES-P.hamadryas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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NCBI_TaxID=9557, 9555;
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                                                                                                                                                                                                                                                          or send an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-97268687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Papio hamadryas (Hamadryas baboon), Papio anubis (Olive baboon).
                                                                                                                                                             EMBL;
                                                                                                                                                                                       EMBL;
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15-JUL-1998 (Rel. 36, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
3-C chemokine_receptor type 5 (C-C CKI
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                                                                                                                                            InterPro;
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sonhuman primates.";
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                                                                                                                                                                                                                                                                                                                                                                      DIFFERENTIATION.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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een the Swiss Institute of Bio
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                                                                                                                                                                       AF105289;
AF105290;
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. Hum. Ret
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0001; 7tm_1; 1.
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                                                                                                                                                                                      ); AAD20558.1;
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                                             MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV
                                                                     HFPYSQYQFWKNFQTLKIVILGLVLFLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI
                              HFPYSQYQFWKNFQTLKIVILGLYLPLLYMYICYSGILKTLLRCRNEKKRHRAVRLIFTI
                                                                                                                           LKSMTDIYLLNLAISDLLFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII
                                                                                            LLTIDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQREGLHYTCSS
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BY SIMILARITY.
SULFATION (BY SIMILARITY N-LINKED (GLCNAC...).
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Pred.
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6 (POTENTIAL
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EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL).
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CYTOPLASMIC (
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CKR5_TRAFR
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AC 099878
DT 30-MAY
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GN CCR5 O
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COM TRACHY
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097878;
30-MAY-2000
30-MAY-2000
15-JUN-2002
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Trachypithecus irancolsi (Francols' langur) (Indochinese langur).
Finkarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Finkarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                          SEQUENCE FROM N.A.

MEDLINE-99416438; PubMed-10486970;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Paguence evolution of the CCR5 chemokine receptor gene
Mol. Biol. Evol. 16:1145-1154(1999).

-IP FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS
-IP FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS
-IP STATE THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATIO
IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATIO
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(Rel. 39, Last sequence update)
(Rel. 41, Last annotation update)
ne_receptor type 5 (C-C CKR-5) (CC-CKR-5)
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    LOCATION: Integral
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RESULT 8
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PROSTTE; PS00237; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; G-protein; G-protein coupled receptor; Transmembrane; Glycoprotein; G-protein; G-p
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CYTOPLASMIC (POTENTIAL).

BY SIMILARITY.

BY SULFATION (BY SIMILARITY).

SULFATION (BY SIMILARITY).

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SULFATION (BY SIMILARITY).
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CYTOPLASMIC (POTENTIAL).
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Pred. No. 2.1e-90;
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                                                           LKSMTDIYLLNLAISDLEFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII
LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS
                                       LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII
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15-JUN-2002 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS: PROUZES, G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50237; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein;

G-protein coupled receptor; Transmembrane; Glycoprotein;

G-protein coupled receptor; Transmembrane; Glycoprotein;

G-protein coupled receptor; Transmembrane; Glycoprotein;
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"Sequence evolution of the CCR5 chemokine receptor
MO1. Biol. Evol. 16:1145-1154(199).
-I- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. B1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-9941643B; PubMed-10486970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED
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Pred. No. 2.3e-90;
6; Mismatches 2
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EXTRACELLULAR
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                                                                                                                                                               EMBL; AF075448; AAD19860.1; -. InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                         Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
"Sequence evolution of the CCR5 chemokine receptor gene in primates.
Mol. Biol. Evol. 16:1145-1154(1999).
-I- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHI
MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCRESSING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
DIFFERENTIATION.
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NCBI_TaxID=54133;
                                                                                                                       G-protein
                                                                                                                                                PRINTS; PR00237; GPCRRHODOPSN
                                                                                                                                                         Pfam; PF00001;
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Mammalia; Eutheria;
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15-JUN-2002 (Rel.
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SIMILARITY: BELONGS TO
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                                                                                                                              PS00237; G_PROTEIN_RECEP_F1_1; PS50262; G_PROTEIN_RECEP_F1_2;
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39,
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Last annotation update)
r type 5 (C-C CKR-5) (CC-
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2 (POTENTIAL
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G-PROTEIN COUPLED RECEPTORS
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Mammalia; Eutheria;
NCBI_TaxID=61853;
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  AAD19863.1;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE=99416438; PubMed=10486970;

Zhang Y.-W., Ryder O.A., Zhang Y.-P.;

Zhang Y.-W., Ryder O.A., Zhang Y.-P.;

Sequence evolution of the CCR5 chemokine receptor gene i

Mol. Biol. Evol. 16:1145-1154(1999)

-I- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO

MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A S

INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY

IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION
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(Rel. 39, Last sequence update)
(Rel. 41, Last annotation updat
ne receptor type 5 (C-C CKR-5) (
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Primates; Catarrhini; Hylobatidae;
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pred. No. 2.3e
7; Mismatches
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RN NO COCO
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Best Local S
Matches 346
CCR5 OR CMKBR5.

Macaca mulatta (Rheaus macaque),
Macaca fascicularis (Crab eating m
Macaca nemestrina (Pig-tailed maca:
Eukaryota; Mctazoa; Chordata; Cran
Mammalis; Euthoris; Primates; Cata
Corcoplithecinae; Macaca.
NCBI_TaxID-9544, 9541, 9545;
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PF00001; 7tm 1· 1
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PS50262; G_PROTEIN_RECEP_F1_2; 1.
PS50262; G_PROTEIN_RECEP_F1_2; 1.
Coupled receptor; Transmembrane; Glycoprotein; Sulfation.
1 30
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                               HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI
                                                                                                                                                                                                                                                                                                                              HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI
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                                                                                                          Last sequence update)
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r type 5 (C-C CKR-5) (CC-CKR-5)
                                                                                                                                                Created)
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2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

4 (POTENTIAL).

5 (POTENTIAL).

5 (POTENTIAL).

6 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

7 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

7 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

7 (POTENTIAL).

SULFATION (BY SIMILARITY).

SULFATION (BY SIMILARITY).

SULFATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1814; DB 1;
Pred. No. 2.6e-90;
                                     macaque).
Craniata; Vertebrata;
Catarrhini; Cercopithe
                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4F8E4F344CEB7C91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                        macaque)
                                                                                                                                                                         352
                                                                                                                                                                       ₿
                                      Cercopithecidae;
                                                                         (Cynomolgus monkey),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 352;
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                                                   Euteleostomi;
                                                                                                           (CCR-5)
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     EMBL; U77672; AAC51109.1; -.
EMBL; U73739; AAC51158.1; -.
EMBL; U73739; AAC34132.1; -.
EMBL; AF005660; AAB62554.1; -.
EMBL; AF005661; AAB62555.1; -.
EMBL; AF005662; AAB62555.1; -.
EMBL; AF005662; AAB62555.1; -.
EMBL; AF005662; AAB62556.1; -.
EMBL; AF005662; AAB62556.1; -.
EMBL; AF005662; AAB62556.1; -.
EMBL; AF005662; AAB62556.1; -.
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  TRANSMEM DOMAIN TRANSMEM
                                    TRANSMEM
DOMAIN
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                                                                                     TRANSMEM DOMAIN
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DOMAIN
                                                                                                                                   PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                            Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M. Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Co Peiper S.C., Parmentier M., Broder C.C., Doms R.W.; "Differential utilization of CCR5 by macrophage and T cel. Simian immunodeficiency virus strains."; Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).

11. FUNCTION, RECEPTOR FOR A C-C TYPE CHEMOKINE, DINDS TO INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=M.mulatta;
MEDLINE=21354176; PubMed=11461684;
Margulies B.J., Hauer D.A., Clements J.E.;
Margulies B.J., Hauer D.A., Clements J.E.;
"Identification and comparison of eleven rhesus macaque chemokine receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES-M.mulatta; STRAIN-Indian macaque;
MEDLINE-97213934; PubMed-9060623;
Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
"Genetically divergent strains of simian immunodeficiency virus
CCR5 as a coreceptor for entry.";
J. Virol. 71:2705-2714(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. SPECIES-M.mulatta; MEDLINE-97184592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES-M.mulatta,
MEDLINE-97268687; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                            PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIDS
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                                                                                                                                                                                                                                                                                                                                               DIFFERENTIATION.

DIFFERENTIATION: Integral membrane protein.

SUBCCELLULAR LOCATION: Integral membrane protein COUPLED RECEPTORS.

SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Res. Hum. Retroviruses 17:981-986(2001).
                                                                                                                               PR00237; GPCRRHODOPSN.

; PS00237; GPROTEIN_RECEP_F1_1; 1.

; PS50262; GPROTEIN_RECEP_F1_2; 1.
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                                                                                                                        receptor;
   30
58
68
102
124
141
198
218
  ; Transmembrane; (
EXTRACELLULAR (
1 (POTENTIAL).
1 (POTENTIAL).
CYTOPLASMIC (PC
2 (POTENTIAL).
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EXTRACELLULAR (
3 (POTENTIAL).
CYTOPLASMIC (PO
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EXTRACELLULAR (
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                                     (POTENTIAL).
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                                                                                                          Glycoprotein; (POTENTIAL).
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062744; 062744; 062745; 062746;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-C Chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DISULFID
                                      Chen Z., Gettie A., Ho D.D., Marx P.A.;
"Primary SIVsm isolates use the CCR5 coreceptor naturally infected in west Africa: a comparison of primary SIVsm, HIV-2, and SIVsmc.";
Virology 246:113-124(1998).
                                                                                SEQUENCE FROM N.A. STRAIN-ISOLATE 079, 085, 087, and MEDLINE-98321155; PubMed-9656999;
                                                                                                                            Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                      CERTO
      <del>-</del>
                                                                                                                       Cercopithecinae; Cercocebus.
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MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A INCREASING THE INTRACELICIAR CALCIUM 10NS LEVEL. MAY IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION DIFFERENTIATION.

SUBCELLULAR LOCATION: Interm?
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use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fc entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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PROSITE; PS00237; G_PROTEIN_RE
PROSITE; PS50262; G_PROTEIN_RE
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MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV
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nilarity 97.48;
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G_PROTEIN_RECEP_F1_2; 1.
G_PROTEIN_RECEP_F1_2; 1.
receptor; Transmembrane; Glycoprotein;
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EXTRACELLULAR (POTENTIAL).
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Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.

1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,

MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY

TNCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an cmail to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U83324; AAC51795.1; -. EMBL; U83325; AAC51796.1; -. EMBL; AB015944; BAA31328.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98001387; PubMed-9343222;
Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.;
"Polymorphisms in the CCR5 genes of African green monke
implicate specific amino acids in infections by simian
immunodeficiency viruses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cercopithecinae;
NCBI_TaxID=9534;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Cercopith
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Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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                                                                                                                                                                                                                                                                                                                                                           PR00237; GPCRRHODOPSN; PS00237; G_PROTEIN_RI
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G_PROTEIN_RECEP_F1_2;
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N_RECEP_F1_2; 1.
; Transmembrane;
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                                                                                            HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI
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CKR5_MOUSE
P51682; 061867; P97405; 035313; P77500; 201-0CT-1996 (Rel. 34, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=129/SvJ; TISSUE-Spleen;
MEDLINE-96205938; PubMed-8631787;
MEDLINE-96205938; PubMed-8631787;
MEDLINE-96205938; PubMed-8631787;
SEQUENCE FROM N.A.

STRAIN-C57BL/6 x CBA; TISSUE-Thymus;
MEDLIXNE-9637B910; PubMed-8662890;
MEDLIXNE-9637B910; PubMed-N662890;
Cloning and characterization of a novel
inflammatory protein-1 alpha receptor.";
J. Biol. Chem. 271:14445-14451(1996).
                                                                                                                                                                           "MOLECULAR cloning and functional expression of murine JE (monocyte chemoattractant protein 1) and murine macrophage inflammatory protein lalpha receptors: evidence for two closely linked C-C chemokine receptors on chromosome 9.";
J. Biol. Chem. 271:7551-7558(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; I
Sciurognathi; Muridae;
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                                                                        Wells
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                                                 .N.C., Powe macrophage
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SEQUENCE FROM N.
STRAIN-129/Ola;
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Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

1. FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SI INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.

1. SUBCELLULAR LOCATION: Integral membrane protein.

1. TISSUE SPECIFICITY: DETECTED IN MONOCYTE/MACROPHAGE CE BUT NOT IN NONHEMATOPOIETIC CELL LINES.
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STRAIN=C57BL/6, and NIH Swiss; TJ
MEDLINE=98001387; PubMed=9343222;
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J. Virol. 71:6305-6314(1997).
[6]
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implicate specific amino acids
immunodeficiency viruses.";
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the European Bioinformatics Institute. These
use by non-profit institutions as long a
modified and this statement is not removed.
entitles requires a license agreement (See
or send an email to license@isb-sib.ch).
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Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M.,
Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W.,
"Two distinct CCR5 domains can mediate coreceptor usage l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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L; X94151; CAA63867.1; ...
L; U68565; AAB37273.1; ...
L; H63327; AAC53386.1; ...
L; AF02990; AAC53389.1; ...
L; AF019772; AAB71183.1; ...
L; AB7019772; AAB71183.1; ...
L; AB7019772; AAB71183.1; ...
L; AB7019772; AAB712024.1; ...
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een the Swiss Institute of Bioinformatics and the Eb
European Bioinformatics Institute. There are no restr
by non-profit institutions as long as its content
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SEQUENCE
                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
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              upregulation of i
J. Neurosci. Res.
                           MEDLINE=98334064; PubMed=9670989; Spleiss O., Gourmala N., Boddeke Spleiss O., Gebicke-Haerter P.J.; Berger M., Gebicke-Haerter P.J.; "Cloning of rat HIV-1-chemokine.
                                                         STRAIN-Wistar;
                                                               SEQUENCE FROM N.A.
                                                                           NCBI_TaxID=10116;
                                                                                                          CCR5 OR CMKBR5
                                                                                                                pha receptor).
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              of rat HIV-1-chemokine coreceptor CKR5 tion of its mRNA in ischemic and endotox sci. Res. 53:16-28(1998).
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(Rel. 39, Last annotation update)
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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EMBL; U77350; AAC03243.1; -.
IntorPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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J. Neuroimmunol. 86:1-12(199)
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Deflebre C.M., Pennell N.A.,
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MEDLINE-98318173; PubMed-9655467;
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81.9%; Pred. No. 4e-76;
tive 27; Mismatches 35; Indels
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CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

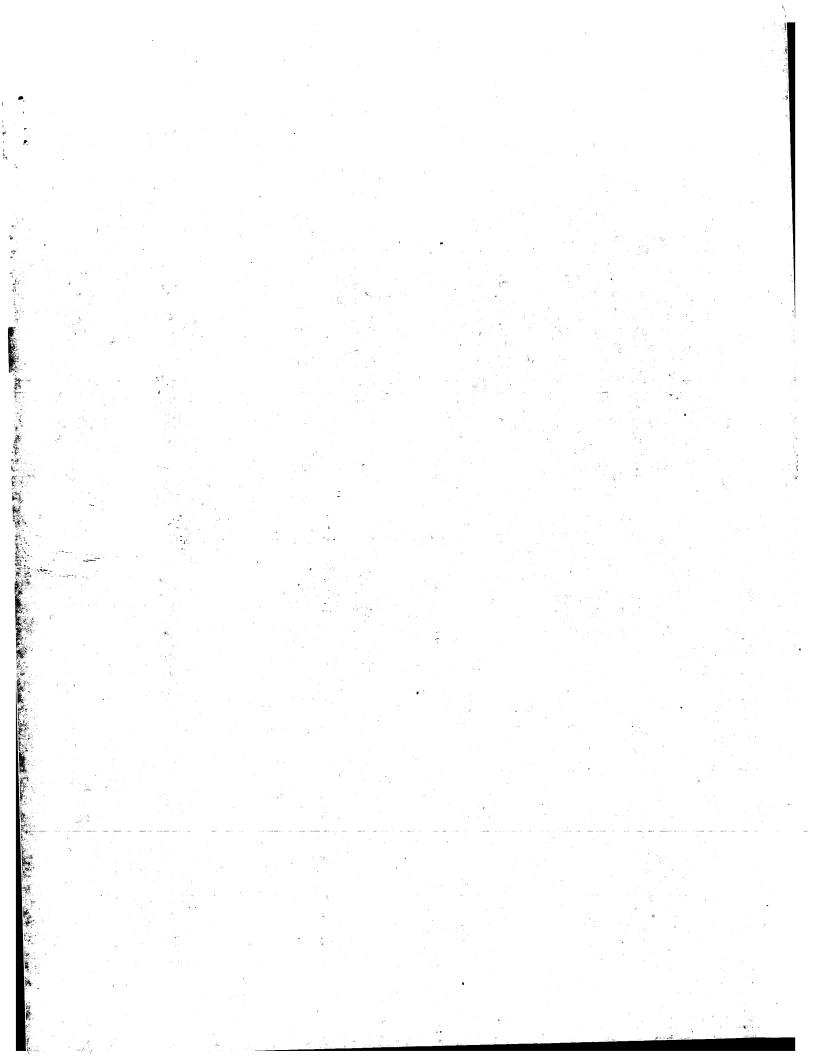
3 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

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Transmembrane; Glycoprotein.
EXTRACELULAR (POTENTIAL).
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Search completed: June Job time : 21.1411 secs



GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd

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61 KSMTDIYLLNIAISDLEFLLTYPEWAHYAAAQWDFGNIMCQLLTGLYFIGEFSGIEFII 120	61 LKSMTDIYLLNLAISDLEELLTVPEWAHYAAAQWDEGNTMCQLLTGLYEIGEESGIEEII 120	1 MDYQVSSPTYDIDYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60	1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60	Query Match 99.1%; Score 1825; DB 6; Length 352; Best Local Similarity 98.9%; Pred. No. 9.5e-147; Matches 348; Conservative 2; Mismatches 2; Indels 0; Gaps 0;	SEQUENCE 352 AA; 40508 MW; F4F64B3AD5AF658A CRC64;	Receptor.	PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.	PROSITE: PS0037; G PROTEIN RECEP F1 1: UNKNOWN 1.	pfam. prococt: 7tm 1: 1	EMBL; AF177884; AAK43367.1; -	Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.	phylogeny.";	"Sequence comparison of the CCR5 gene in primates and primate	Zhang Y., Ryder O.A., Zhang Y.;	SEQUENCE FROM N.A.	(1)		Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Hylobates syndactylus (Siamang) (Symphalangus syndactylus).	CCR5.	ne receptor 5.	(TrEMBLrel. 20,	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)	-2001		Q95NC5 PRELIMINARY; PRT; 352 AA.	ניז 1 כיז

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RESULT
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PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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STRAIN-CHCCR5-141A;
Zhang L., Carruthers
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Mammalia; Eutheria;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Mammalia; Eutheria;
NCBI_TaxID=9598;
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352 AA;
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R Pfam; pF00001; 7tm_1; 1.

PFINTS; PR00237; GPCRRHODDSN.
PROSITE; PS00237; GPCRRHODDSN.
PROSITE; PS00237; G_PROTETN

PROSITE; PS00237; G_PROTETN
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Gorilla gorilla (gorilla).
Eukaryota; Metazoa; Chordata;
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                            (TrEMBLrel.) (TrEMBLrel...) (TrEMBLrel...) (TrEMBLrel...)
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G_PROTEIN_RECEP_F1_2;
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Pred. No. 1.4e-146;
3; Mismatches 1;
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Best Local :
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MEDLINE-99210133; PubMed-10195758;

Saksena N.K., Wang B., Novembre F.J., Bolton W.,

Species specific changes in the CCR5 gene from
nonhuman primates ";
AIDS Res. Hum. Retroviruses 15:479-483(1999).

EMBL; AF105291; AAD20560.1; -.

InterPro; IPR000276; GPCR_Rhodpsn.

Pfcns; PF00001; 7tm_l; 1.

Pfcns; PF00001; 7tm_l; 1.

PRINTS; PR00237; GPROTEIN_RECEP_F1_1; UNKNOWN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
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OSTV50:
O1-MAY-2000 (TrEMBLrel. 13, C.
O1-MAY-2000 (TrEMBLrel. 13, L.
O1-JUN-2001 (TrEMBLrel. 17, L.
CC chemokine receptor type 5.
CCR5.
                                                                 MEDITINE-99335215; PubMed-10408730; Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Cour Muller-Trutwin M.C., Corbet S., Hansen J., Fomsgaard A.; Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.; **Mutations in CGFS-coding sequences are not associated carrior status in African nonhuman primates.**; AIDS Res. Hum. Retroviruses 15:931-939(1999).
                                                                                                                                                                                                                                                                                           Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Primates;
    SEQUENCE FROM STRAIN-1410;
                                                                                                                                                                                                     STRAIN-1410;
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                   NCBI_TaxID=9598;
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NCBI_TaxID-9593;
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Catarrhini; Hominidae
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                                                                                                                                    Fomsgaard A.;
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and Asian
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MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR

Query Match Best Local S Matches 347

Similarity

98.8%;

Score 1818; DI Pred. No. 3.7e 2; Mismatches

.7e-146;

DB 6;

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9623CA98340CF274 CRC64;

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Best Local S
Matches 346
                              SEQUENCE FROM N.A. Zhang Y.;

**2 Zhang Y., Ryder O.A., Zhang Y.;

**2 Zhang Y., Ryder O.A., Zhang Y.;

**Sequence comparison of the CCR5 gene in primates and Phylogeny.*;

L Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databas R EMBL; AF177899; AAK43382.1; -..

R InterPro; IPR000276; GPCR_Rhodpsn.

R Pfam; pF00001; 7tm.1; 1.

R PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.

R PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Q95NCO;
01-DEC-2001
PROSITE; |
PROSITE; |
Receptor.
SEQUENCE
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Georges-Courbot M.-C., Barre-Sinoussi F., Fons
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ
EMBL; AF035214; AAD44007.1; -
InterPro; IPR000276; GPCR_Rhodpsn.
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prints: pr00237; GPCRRHODOPSN.
pr0SITE: pS00237; G_PROTEIN_RECEP_F1_1;
pr0SITE: pS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                 Hylobates moloch (silvery gibbon).
Eukaryota; Metazoa; Chordata; Craniata; V.
Mammalia; Eutheria; Primates; Catarrhini;
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Pred. No. 2.1e
5; Mismatches
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Q95NC7;
Q1-DEC-2001
Q1-DEC-2001
Q1-MAR-2002
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Zhang Y., Ryder O.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nasalis larvatus (Proboscis monkey).
Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Eutheria; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                    SEQUENCE
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 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV
                            GEKFRNYLLVFFQKHIAKHFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL
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(Tremblrel. 19, Last sequence (Tremblrel. 20, Last annual receptor 5.
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97.7%;
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Pred. No. 4.5e-146;
7; Mismatches 1;
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ecidae; Colobinae;
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"Sequence comparison of the CCR5 gene in phylogeny.";
phylogeny.";
Submitted (AUG-1999) to the EMBL/GenBank/E
EMBL; AF177881; AAK43364.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pf000001; 7tml_i 1
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UN
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
O97962;
01-MAY-1999 (TIEMBLTel. 10, Created)
01-MAY-1999 (TIEMBLTEL. 10, Last sequence up
01-JUN-2001 (TIEMBLTEL. 17, Last annotation
C-C chemokine receptor type 5.
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Mammalia; Eutheria;
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DEC-2001 (TrembLrel. 1)
MAR-2002 (TrembLrel. 2)
chemokine receptor 5.
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Primates;
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Pred. No. 5
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                                                                                                                                                                                                                                                                                                              Q9XT14;
Q9XT14;
01-NOV-1999
01-NOV-1999
01-DEC-2001
                     SEQUENCE FROM N.A.

Spearman P.W., Mburu D.N., Graham B.S.;

Spearman P.W., Mburu D.N., Graham B.S.;

**Dlifferential Utilization of CCR5 Molecules from Three Simian Species by the HIV-1 Envelope Glycoprotein.";

Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF141639; AAD32684.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sequence evolution of chemo submitted (JUN-1998) to the EMBL; AF075447; AAD19859.1; EMBL; AF075444; AAD19856.1;
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Pfam; PP00001; 7tm_1; 1.

PRINTS; PR00237; GPCRRHDODPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.

PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
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Mammalia; Eutheria;
                                                                                                                                                                    NCBI_TaxID-33548;
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NCBI_TaxID=66062,
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(golden sni
Chordata; (
Primates; (
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GPCR_Rhodpsn
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the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                            , Created)
, Last sequence up
, Last annotation
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snub-nosed monkey).
srub-nosed monkey).
s; Cranlata; Vertebrata; Euteleostomi;
s; Catarrhini; Cercopithecidae; Colobir
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Pred. No. 9.8e-146;
7; Mismatches 2;
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Craniata; Vertebrata;
Catarrhini; Cercopithe
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PRINTS; P
PROSITE;
PROSITE;
                                                                                                                                                     SEQUENCE
                                                                                                                                                                                       InterPro; IPR000276; GPCR_Rhodpsn

Pfam; PF00001; 7tm_1; 1.

PROSITE; PS00237; G_PROTEIN_RECEP.

PROSITE; PS50262; G_PROTEIN_RECEP.
                                                                                                                                                                                                                                                                                                                                                                                                    Theropithecus gelada (Gelada baboon).
Eukaryota; Metazoa; Chordata; Craniata; V.
Mammalia; Eutheria; Primates; Catarrhini;
Cercopithecinae; Theropithecus.
NCBI_TaxID-9565;
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SEQUENCE
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submitted (AUG-1999) to the
EMBL; AF177891; AAK43374.1;
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343; Conser
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;; PS00237; G_PROTEIN_RECEP_F1_1;
;; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                               Similarity
                     MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR
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G_PROTEIN_RECEP_F1_2;
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pred. No. 1.2e
5; Mismatches
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Pred. No. 1
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Zhang Y., Ryder O.A., 2
"Sequence comparison of
phylogeny.";
Submitted (AUG-1999) to
EMBL; AF177883; AAK433
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01-DEC-2001
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NCBI_TaxID=66063;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Mammalia; Eutheria;
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chemokine receptor 5.
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AR177883; AAK43366.; -.
Pro; IPR000276; GpCk_Rhodpsn.
PF00001; 7tm_1; 1.
PF00237; G_PROTEIN_RECEP_F1_1; UNKNOW
TE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
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                                                                                                                                                                                                                                                                                                                     h 98.4%;
Similarity 97.4%;
43; Conservative
                                                                                                                                           LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII
                                                                                                                                                                                                                    LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII
                                                                                                                                                                                                                                                           GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL
                                              MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV
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                                                                                                                                                                                                                                                                                                                                                                               40462 MW;
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of the
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Last sequence update)
Last annotation update)
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Pred. No. 1.5e-145;
7; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   leaf monkey).
Craniata; Vertebrata; Euteleostomi;
Catarrhini; Cercopithecidae; Colobi
                                                                                                                                                                                                                                                                                                                                                                               52824E0322559F7F CRC64;
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ID Q9XT13
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Best Local S
Matches 344
                                         Q9XT13;
Q9XT13;
01-NOV-1999
01-NOV-1999
01-JUN-2001
CC chemokine
CCR5.
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01-DEC-2001
01-DEC-2001
01-MAR-2002
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SEQUENCE
Papio anubis (Olive
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (AUG-1999) to the EMBL/CEMBL; AF177886; AAK43369.1; IRRO0276; GPC_Rhodpsn Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. Zhang Y., Ryder O.A., "Sequence comparison of phylogeny.";
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PROSITE; PS50262;
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(TrEMBLrel.)
(TrEMBLrel.)
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Chordata;
Primates;
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97.7%;
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CCR5
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Craniata; V. Catarrhini;
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Miopithecus talapoin (Talapoin) (Cercopithecus talapoin).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Miopithecus.

NCBI_TaxID=36231;
                                                                                                                      LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS
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                                                                                                                                                                              MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV
                                                                                                                                                                                           MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV
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AAK43369.1; -.
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.G_PROTEIN_RECEP_F1_2;
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Pred. No. 1.5e
5; Mismatches
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Last sequence up
Last annotation
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sequence update) annotation updat
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Vertebrata;

Euteleostomí;

Cercopithecidae

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Best Local S
Matches 344
 "HIV-1 Bubtypes, co-receptor usage, and CC AIDS Res. Hum. Retroviruses 0:0-0(1997).

EMBL; AF011538; AAB65738.1; -.

Interpro; IPR000276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm_1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; GPCRTHODOPSN.

PROSITE; PS00237; GPCRTHODOPSN.

ROCEPTO:.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spearman P.W., Mburu D.N., Graham B.S.;

**Differential Utilization of CCR5 Molecules from Three E
**Simian Species by the HIV-1 Envelope Glycoprotein.*;

Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AP141640; AAD32685.1; -.

InterPro; IPR000276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm_1; 1.

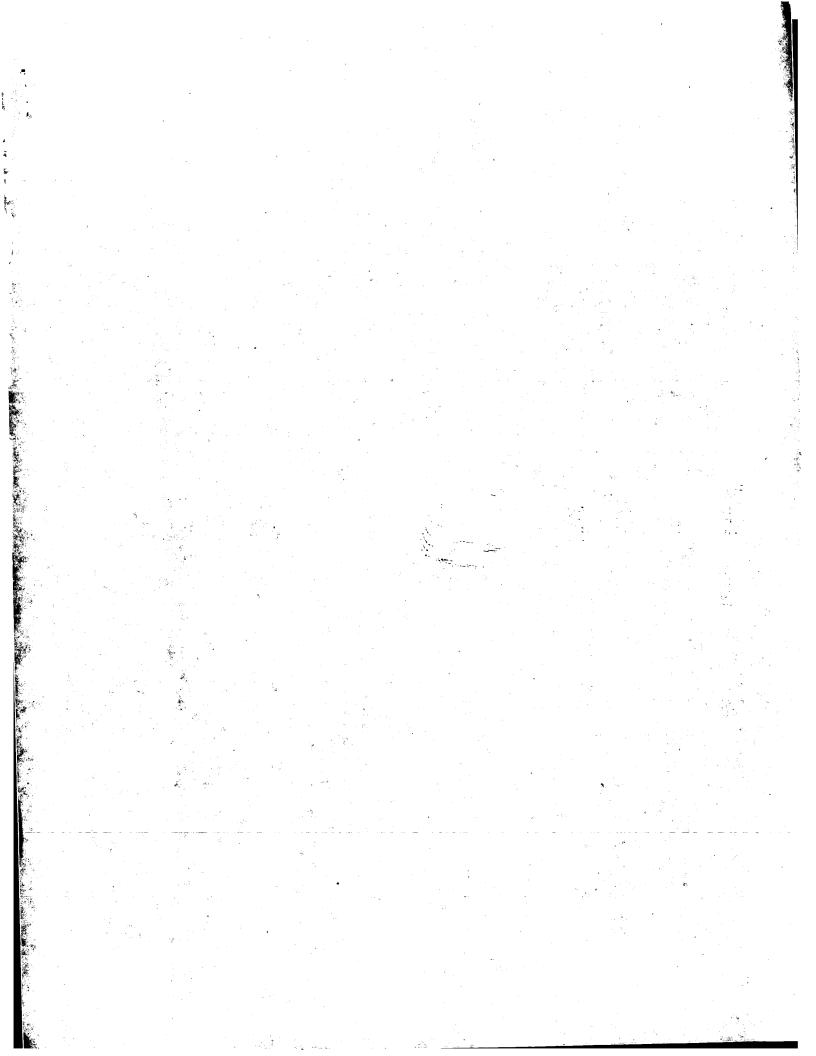
PROSITE; PR00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
PROSITE;
PROSITE;
Receptor.
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Spearman P.W., Mburu D.N.,
"Differential Utilization"
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NCBI_TaxID=9555;
[1]
                                                                                                                 SEQUENCE FROM N.A.
STRAIN-MACCR5-140A;
                                                                                                                                              Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata;
Mammaila; Eutheria; Primates;
NCBI_TaxID=9598;
                                                                                                                                                                                                            01-JAN-1998 (TREMBLIGE) 05,
01-JAN-1998 (TREMBLIGE) 05,
01-DEC-2001 (TREMBLIGE) 19,
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                                                                                                      L., Carruthers C.D.,
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al Similarity 97.7%;
344; Conservative
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                                                                                                      Не Т.,
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pred. No. 2.1e-145;
5; Mismatches 3;
                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation updat
                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Pan.
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Molecules from Three East
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                                                                                                                                             1 Similarity
343; Conserv
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                                                                                                                    MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV
                                              LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS
                                                                                              MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSCNRLDQAMQVT@TLGNTHCCINPIIYAFV
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352 AA;
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                                                                                                                                                                     40523 MW;
                                                                                                                                                   98.28;
97.48;
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                                                                                                                                                   Score 1808;
Pred. No. 2.
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                                                                                                                                             Mismatches
                                                                                                                                            DB 6;
8.6e-145;
les 3;
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Search completed: June 3, 2003, 15:21:41 Job time: 75.8765 secs

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20, Appl 3, Appl 3, Appli 3, Appli 7, Appli 9, Appli 9, Appli 9, Appli 9, Appli 19, Appli

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Perfect score:
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       No. is the number of results predicted by chance greater than or equal to the score of the result a derived by analysis of the total score distributes.
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1: /cgn2_6/ptodata/l/pubpaa/U
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3: /cgn2_6/ptodata/l/pubpaa/U
4: /cgn2_6/ptodata/l/pubpaa/U
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6: /cgn2_6/ptodata/l/pubpaa/U
6: /cgn2_6/ptodata/l/pubpaa/U
9: /cgn2_6/ptodata/l/pubpaa/U
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10: /cgn2_6/ptodata/l/pubpaa/U
11: /cgn2_6/ptodata/l/pubpaa/U
13: /cgn2_6/ptodata/l/pubpaa/I
13: /cgn2_6/ptodata/l/pubpaa/I
13: /cgn2_6/ptodata/l/pubpaa/I
14: /cgn2_6/ptodata/l/pubpaa/I
15: /cgn2_6/ptodata/l/pubpaa/I
16: /cgn2_6/ptodata/l/pubpaa/I
17: /cgn2_6/ptodata/l/pubpaa/I
18: /cgn2_6/ptodata/l/pubpaa/I
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1841
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Maximum Match 100%
Listing first 45 summaries
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./cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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./cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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Copyright (c) 1993 - 2003 Compugen
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9 US-10-086-814-1
9 US-09-734-221A-14
19 US-09-739-841-2
10 US-09-759-823-15
10 US-09-98-719-5
10 US-09-938-703-5
10 US-09-938-703-5
10 US-09-938-703-5
10 US-09-938-703-2
10 US-09-938-703-2
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10 US-09-725-285-2
10 US-09-725-285-2
10 US-09-725-285-2
10 US-09-725-285-2
10 US-09-725-862A-2
10 US-09-79-879A-2
10 US-09-79-879A-2
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Publication No. US20030092632A1
GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William C.
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 61010-AB-1
CURRENT APPLICATION NUMBER: US/10/086,814
CURRENT FILING DATE: 2002-02-28
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 352
TYDE: PRT
TYDE: PRT
ORGANISM: Homo sapiens
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US-10-086-814-1
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Best Local Similarity
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                                              241 MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV
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ilarity 100.0%;
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0 US-99-104-792-3

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0 US-99-104-792-7

0 US-99-131-827A-2

0 US-99-138-703-7

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0 US-99-779-889A-9

10 US-99-779-889A-9

10 US-99-195-662A-9

10 US-99-915-662A-9

10 US-99-915-662A-9

10 US-99-916-247-1

10 US-99-916-547-1

10 US-99-938-713-9

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Pred. No. 1.8e-150;
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US-09-734-221A-14
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                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                              NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-004 N2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/666,020
FILING DATE: 19-JUN-1996
APPLICATION NUMBER: US 08/227,319
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 07601
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                 ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                    HYPOTHETICAL: NO
                                                                                                                                  352;
               61 LKSMTDIYLLNLAISDLFFLLIVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
                                                                                  1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR
                                                               1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR
                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII
                                                                                                                                                                                                                                                                                                                LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/734,221A FILING DATE: 11-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
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                                                                                                                                  Conservative
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                                                                                                                                                                                                                     SEQ ID NO: 14:
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                                                                                                                                                  Score 1841; DB 9;
Pred. No. 1.8e-150;
                                                                                                                                  Mismatches
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SEQ ID NO 2
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Best Local
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TITLE OF INVENTION: Assay Met
FILE REFERENCE: PC10348APMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-(PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/759,841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE:
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ORGANISM: Homo
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                                     GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL
                                                       GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL
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Dobbs, Susan
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Conservative 0
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BER: GB_0000661.9
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                       GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL
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                                                                                  MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV
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1 MDYQVSSPIYDINYYTSEPCQKINYKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60 Score 1841; DB 10; Pred. No. 1.8e-150; DB 10; Indels Length 352; 0; Gaps 60

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; ORGANISM: Homo sapiens
US-09-813-653-15
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                                                                                                                     Sequence 1, Application US/09796202

Patent No. US20020068813A1

GENERAL INFORMATION:

APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/61010/JPW/SHS
CURRENT APPLICATION NUMBER: US/09/796,202

CURRENT FILING DATE: 2001-02-28
                                                           NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn versi
SEQ ID NO 1
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: See, Raymond
APPLICANT: Tan Hehir, Christina
APPLICANT: Tan Hehir, Christina
TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
FILE REFERENCE: CNS-005
FILE REFERENCE: CNS-005
CURRENT APPLICATION NUMBER: US/09/813,653
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: US 60/190,946
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/190,996
PRIOR FILING DATE: 2000-03-21
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                      LENGTH: 352
TYPE: PRT
ORGANISM: human
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                                                                                    version 3.0
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US-09-938-719-5
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Patent No. US20020106742A1
GENERAL INFORMATION:
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Best Local
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                                                                                    REFERENCE/DOCKET NUMBER: INFORMATION: FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0,

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RE
                                                                                                             APPLICATION NUMBER: 09/626,939
FILING DATE: 27-JULY-2000
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, N
STREET: 620 Newport
                                                                                                                                                                                        PRIOR
                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                     APPLICATION NUMBER: US/09/938,719
FILING DATE: 24-Aug-2001
CLASSIFICATION: CUNKNOWN>
R APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                     CITY: Newport Beach
STATE: CA
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                                         TYPE: amino acids
                           TOPOLOGY: linear
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TYPE: protein DESCRIPTION: 9
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SEQ
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t Center Drive
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Pred. No. 1.8e-150;
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                                                                                                    <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                         16th Floor
                                                                                                                                                                                                                                                               Version #1.25 (EPO)
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RESULT 7
US-09-939-226-5
; Sequence 5, Application US/09939226
; Patent No. US20020110805A1
; GENERAL INFORMATION:
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                                                                                                                                              REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PETENTENT Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
FIGURE FLORE FLORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID
                           MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
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                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
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                                                    TOPOLOGY: linear
                                                                                          TYPE:
                                                                                                                                                                                                                                     NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 09/626,939 FILING DATE: 2000-07-27
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STATE: CA
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                                                                                                                      LENGTH: 352 amino acids
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                               TYPE:
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                                                                                          amino acid
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LIBERT, FREDERICK
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Pred. No. 1.8e-150;
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   NO:
                                                                                                                                                                                                                <Unknown>
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US-09-938-703-5
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Patent No. US2002011.0870A1
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 352;
                                                                                                                                                                                 INFORMATION
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                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                              MATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
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LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
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                                                       TOPOLOGY: linear
                                                                                          TYPE:
                                                                                                                                                                                                                                        NAME: Altman, Daniel E REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: <Unknown>
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                                                                                                                         LENGTH: 352 amino acids
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TYPE: protein DESCRIPTION: SEQ
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Pred. No. 1.8e-150;
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Query Match Best Local (

Matches

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RESULT 9
US-10-106-623-2
; Sequence 2, Application US/10106623
; Patent NO. US20020150888A1
; PATENT NFORMATION:
; GENERAL INFORMATION:
               APPLICATION NUMBER: 08/771,276

APPLICATION NUMBER: 08/771,276

FILING DATE: <UNKNOWN>

ATTORNEY/AGENT INFORMATION:

NAME: NO. US20020150888Aland, Greta E.
REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27866/33670

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300

TELEPHONE: 312-474-6300

TELEFAX: 312-474-6448

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/106,623
FILING DATE: 26-Mar-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Raport, Carol J.
TITLE OF INVENTION: Chemokine Receptor Materials NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gray, Patrick W. Schweickart, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
     MOLECULE
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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STATE: Illinois
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                                                                                                                                                                                                                                                   APPLICATION DATA:
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Pred. No. 1.8e-150;
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; TYPE: PRT
; ORGANISM: Homo s
US-09-813-653-17
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OTHER INFORMATION: /- *88C amino;
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-106-623-2
                                                                                                                                                                                                                                                                                         APPLICANT: See, Raymond
APPLICANT: Ten Hehlr, Christina
TITLE OF INVENTION: Binding Compounds and Methods For
FILE REFERENCE: CNS-005
CURRENT APPLICATION NUMBER: US/09/813,653
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: US 60/190,946
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/190,996
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/191,299
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
NUMBER: OS 60/191,299
PRIOR FILING DATE: 2000-03-21
NUMBER: OS 50/191,299
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                                                                                                                                                                                                                                             NUMBER: Pater
SOFTWARE: Pater
; SEQ ID NO 17
FONGTH: 352
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Best Local Similarity
Matches 351; Conserv
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Best Local Similarity
Matches 352; Conserv
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Pred. No. 5.8e-150;
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Pred. No. 1.8e-150;
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US-10-232-686-2
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                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 2
LENGTH: 3
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PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 09/15,662
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 08/466,343
PRIOR FILING DATE: 1995-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human G-Protein Chemokine Receptor
FILE REFERENCE: 1488.115000N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/232,686
CURRENT FILING DATE: 2002-09-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Li, Yi APPLICANT: Ruben,
                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
                                                                                                                         HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI
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                                                       MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV
                                                                   MIVYELFWAPYNIVLLLUTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV 300
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                                                                                                         HFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI
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99.78;
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Pred. No. 8.6e-150;
0; Mismatches 1;
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RESULT 12

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; OTHER INFORMATION: Deduced Amino Acid Sequence US-09-725-285-2
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APPLICANT: L1, Yi
APPLICANT: Ruben, Steven, M.
APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Human G-protein Chemokine Rec
FILE REFERENCE: 1488.115000A
CURRENT APPLICATION NUMBER: US.09/779,879A
CURRENT FILLING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,258
PRIOR APPLICATION NUMBER: US 60/181,999
PRIOR APPLICATION NUMBER: US 60/187,999
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LENGTH: 352
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APPLICANT: Li, Yi
APPLICANT: Ruben, Steven,
                                                                                                                                                                                                                                            Sequence 22, Application US/09779879A Patent No. US20020048786A1
                                                                                                                                                                                                                               GENERAL INFORMATION:
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Best Local Similarity
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TITLE OF INVENTION: ANGLE-TOTAL TITLE OF INVENTION: (CCR5 Receptor)
TITLE OF INVENTION: 1488.1150003
TOTAL DEPTRENCE: 1488.1150003
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                                                                                                                                                                                         APPLICANT: Rosen, APPLICANT: Rosch
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1995-06-06
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Pred. No. 8.6e
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8.6e-150;
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US-09-779-880A-22
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TITLE OF INVENTION: Human G-protein Chemokine Rec
FILE REFERENCE: 1488.115000C
CURRENT APPLICATION NUMBER: US/09/779,880A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,258
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/187,999
PRIOR APPLICATION NUMBER: US 60/187,999
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEO ID NOS: 58
ROPTMANE: DATE: 2000-09-22
NUMBER OF SEO ID NOS: 58
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Best Local S
Matches 351
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PRIOR FILING DATE: 2000-99-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PATCHITIN VORSION 3.0
SEQ ID NO 22
LENGTH: 352
TYPE: PRT
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Best Local S
Matches 351
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                                                                                                                                           SOFTWARE: PatentIn version 3.0 SEQ ID NO 22 LENGTH: 352
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Pred. No. 8.6e-150;
Namatches 1;
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3.6e-150;
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US-09-195-662A-2
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SEQ ID NO 2
LENGTH: 352
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Best Local S
Matches 351
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CURRENT EILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 08/4:
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
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APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Human G
FILE REFERENCE: 1488.115000
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                                                                                                                                    HEPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTI
 GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTEEQEISVGL
                                                                    MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV
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                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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1488.115000
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Pred. No. 8.6e-150;
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Search completed: June 3, 2003, 15:34:30 Job time : 46.6279 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                      Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
Match
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Gapop 10.0 , Gapext 0.5
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/cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USIO_NEM_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/USIO_NEM_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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                        US-10-086-814-1
US-09-734-221A-14
0 US-09-725-285-2
0 US-09-759-841-2
0 US-09-779-880A-22
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0 US-09-813-653-15
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0 US-09-813-652-1
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US-09-939-728-6
US-09-938-703-6
US-09-938-719-4
US-09-938-703-6
US-09-938-703-6
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                      14, Appl
2, Appl
2, Appl
22, Appl
22, Appl
15, Appl
11, Appl
11, Appl
12, Appl
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	52.9	52.9	52.9	53.3	53.3	53.3	54.2	54.2	54.2	54.2	61.7	61.7	61.7	61.9	61.9				61.9			84.0			85.4	85.4
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	05-09-938-703-9	US-09-939-226-9	US-09-938-719-9	US-10-219-834-78	US-09-960-547-1	-961	US-09-502-783A-9	-09-339-912A-	-09-195	9	69	US-09-939-226-7	US-09-938-719-7	US-09-131-827A-2	us-09-104-792-3	US-09-779-880A-9	US-09-779-879A-9	US-10-232-686-9	ÿS-09-131-827A-20	US-10-106-623-20	US-09-779-880A-2	US-09-779-879A-2	US-09-813-653-17	US-10-106-623-2	US-09-502-783A-2	US-09-938-703-5
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ALIGNMENTS

RESULT 1 US-09-938-719-6

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Sequence 6, Application US/09938719
Patent No. US20020106742A1
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT
LIBERT FREDBERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESSEE: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORPUSESSEE: KNOBBO, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
COUNTRY: U.S.A.
COUNTRY: U.S.A.
COUNTRY: U.S.A.
COUNTIER READABLE FORM:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION: CURRENT NEW APPLICATION NUMBER: US/09/938,719
FILING DATE: 27-ULY-2000
ATTONELLING DATE: 27-ULY-2000
ATTONELLING DATE: 27-ULY-2000
ATTONELLING DATE: 27-ULY-2000
ATTONELLING DATE: 127-ULY-2000
ATTONELLING DATE: 127-ULY-2000
ATTONELLING DATE: 100-16
SEQUENCE CHARACTERISTICS:
LENGTH: 215 sanino acids
TYPE: ammino acids
TYPE: ammino acids
TYPE: mino acids
TYPE: mino acids
TYPE: mino acids
TYPE: mino acids
TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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                                                                            Query Match
Best Local :
                                                          Matches
                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: 6:
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                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR AND NUCLEIC ACID MOLECULES ENCODING SAID R
                                                                                                                                                    MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
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STREET: 620 Newport Center Drive 16th Floor
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Pred. No. 4.2e-104;
; Mismatches 0;
                                                          Score 1122; DB 10;
Pred. No. 4.2e-104;
); Mismatches 0;
                                                                                                                                                                                                                                                                                             <Unknown>
                                                            Indels
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US-09-938-703-6
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                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA
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                                                                                  LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
                                                                                                                                                              MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09938703
        LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS
                                                              LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII
                                                                                                                                                                                                                                                                                                                                                   LENGTH: 215 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 09/626,939 FILING DATE: 2000-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 24-Aug-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 620 Newport Center Drive
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                                                                                                                                        MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                     Conservative
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LIBERT, FREDERICK
LIBERT, FREDERICK
INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RI
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                                                                                                                                                                                                                                     100.0%;
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                                                                                                                                                                                                                     Score 1122; DB 10;
Pred. No. 4.2e-104;
; Mismatches 0;
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SAID RECEPTOR

Indels Length

Gaps

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; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ US-09-938-719-4
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    RESULT 5
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 09/626,939
FILING DATE: 27-JULY-2000
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/938,719
FILING DATE: 24-Aug-2001
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
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LIBERT, FREDERICK
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                             MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
                                                                                                     HFPY 184
                                                                                                                                               LTIDRYLAVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS
                                                                                                                                                                                      LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                                                                                                                                                                                                                                 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTMARE: PATCHTH Release #1.0, Version #1.25 ENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SENGTH: 184 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                             Score 958; DB 10;
; Pred. No. 7.5e-88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 184;
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US-09-938-703-4
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                                                          Sequence 4, Application US/09938703
Patent No. US20020110870A1
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/939,226

FILING DATE: 24-Aug-2001

CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
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NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
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PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
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                                                                                                                                                                                                                                                                                                                                  121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                                                                                                                                                                                                                               181 HFPY 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.4%; Score 958; DB 10; ilarity 100.0%; Pred. No. 7.5e-88; Conservative 0; Mismatches 0;
: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
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RESULT 7
US-10-232-686-2
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PRIOR APPLICATION NUMBER: 09/339,912
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 09/339,912
PRIOR APPLICATION NUMBER: 09/195,662
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 08/466,343
PRIOR FILING DATE: 1995-06-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                   Sequence 2, Application US/10232686 publication No. US20030023044A1
                                                                                                                                      APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGNR10
FILE REFERENCE: 1488.115000N
CURRENT APPLICATION NUMBER: US/10/232,686
CURRENT FILING DATE: 2002-09-03
                                                                                                                                                                                                                           APPLICANT: Li, Yi APPLICANT: Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 09/626,939 FILING DATE: 2000-07-27 ATTORNEY/AGENT INFORMATION:
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STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
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REGISTRATION NUMBER: 34,115
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Pred. No. 7.5e-88;
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Sequence 14, Application US/09734221A Publication No. US20030096221A1

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-232-686-2
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US-10-086-814-1
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US-10-086-814-1
RESULT 9
US-09-734-221A-14
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THICKH: 352
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Best Local S
Matches 184
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Best Local Similarity
Matches 184; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William C.
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 61010-AB-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/086,814
CURRENT FILING DATE: 2002-02-28
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84; Conservative
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-004 N2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPHONE: 201-487-5804
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/734,221A
FILING DATE: 11-Dec-2000
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/666,020
FILING DATE: 19-JUN-1996
APPLICATION NUMBER: US 08/227,319
FILING DATE: 13-APR-1994
                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens SEQUENCE DESCRIPTION: SEQ ID NO: 14:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza,
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                                                                    HFPY 184
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                                   HFPY 184
                                                                                                         LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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MACROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
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100.0%; Pred. No. 1.6e-87;
tive 0; Mismatches 0;
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US-09-725-285-2
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                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09759841 Patent No. US20010039026A1
                                                SOFTWARE:
SEQ ID NO 2
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                                                                                                                                                                                               APPLICANT: Dobbs, Susan
APPLICANT: Perros, Manoussos
TITLE OF INVENTION: Assay Method
FILE REFERENCE: PC10348APME
CURRENT APPLICATION NUMBER: US/09/759,841
CURRENT FILING DATE: 2001-01-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                   PRIOR FILING DATE: 2000-PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-
                                                                                                                                                    PRIOR APPLICATION NUMBER: GB 0000661.9 PRIOR FILING DATE: 2000-01-12 PRIOR APPLICATION NUMBER: GB 0000663.5
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PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 08/
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CURRENT FILING DATE: 2000-11-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1999
                                                                                    NUMBER OF SEQ ID NOS:
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TYPE: PRT
ORGANISM: Artificial Sequence: Genomic
                LENGTH: 352
TYPE: PRT
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ORGANISM: Homo sapiens
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                                                                    PatentIn Ver.
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                                                                                                                                                                                                                                                                                                               Rickett, Graham A
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                                                                                                                     GB 0000659.3
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US-09-759-841-2

Length 352;

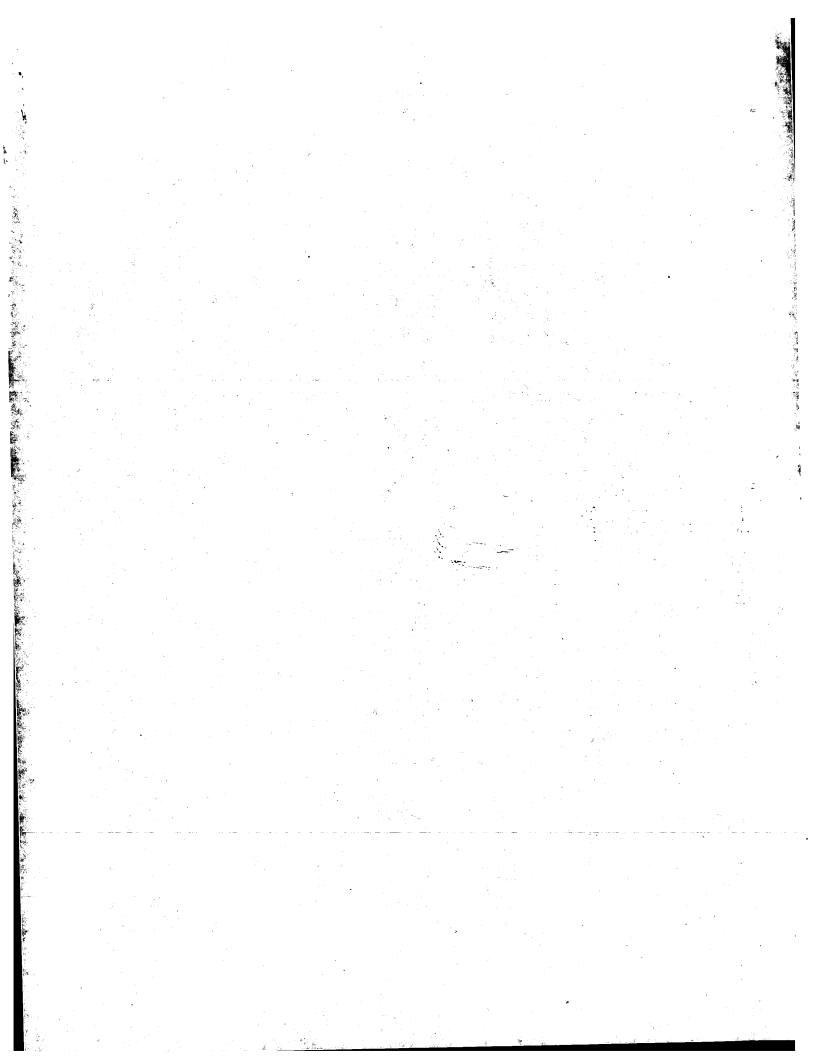
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US:09-779-879A-22
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RESULT 13
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Best Local Similarity
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LENGTH: 352
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NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
FILE REFERENCE: 1488.115000A
CURRENT APPLICATION NUMBER: US/09/779,879A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,258
PRIOR FILING DATE: 2000-02-09
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PRIOR FILING DATE: 2000-03-09
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                     Local Similarity
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pred. No. 1.6e-87;
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US-09-813-653-15
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ORGANISM: Homo sapiens US-09-813-653-15
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patent No. US20020064770A1
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PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: US 60/187,999
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/234,336
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
                                                                                   SEQ ID NO 15
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TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
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CURRENT FILING DATE: 2001-03-20
                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/190,946
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/190,996
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                     APPLICANT: See, Raymond APPLICANT: Tan Hehir, Christina APPLICANT: Tan Hehir, Christina TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compound FILE REFERENCE: CNS-005
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Nestor, John APPLICANT: Wilson, Carol
                                                                                                                      PRIOR APPLICATION NUMBER: US 60/191,299 PRIOR FILING DATE: 2000-03-21 NUMBER OF SEQ ID NOS: 44
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Local Similarity 100.0%; Pred. No. 1.6e-87;
hes 184; Conservative 0; Mismatches 0;
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Sequence 1, Application US/09796202

Patent No. US20020068813A1

GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/61010/JPW/SHS
CURRENT APPLICATION NUMBER: US/09/796,202
CURRENT FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 17
SOSTWARE: Patentin version 3.0
SEQ ID NO 1
LENCTH: 352
TYPE: PRT
ORGANISM: human
US-09-796-202-1
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100.0%; Pred. No. 1.6e-87;
tive 0; Mismatches 0;
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Maximum DB seq length: 2000000000
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SUMMARIES

WPI; 1997-479829/44

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2	AAB0037/	,	ָ מ מ		7 1
Rat CC chemokine r	J	18	355	50.4	
Human CC-chemokine	AAB20571	21	355	53.3	598
Human MIP-lalpha/R	AAW25751	18	355	53.3	598
Human MIP-1 alpha/	t.n	18	355	53.3	598
3	AAR52749	15	355	•	598
Human MCP-1 recept	AAB46859	22	329	54.2	608.5
Human CCR2a protei	AAG80107	22	. 374	•	694
Human monocyte che	AAR79165	16	374	61.9	694
Human wild-type CC	AAU07614	22	360	•	694
Human CCR2b prote1	AAG80108	22	360	•	694
Non-endogenous hum	ABB56340	22	360	61.9	694
Human monocyte che	AAW35833	18	360	•	694
	AAR79166	16	360	•	694
Human CCR2-64I pol	AAU07613	22	360	•	695
Mouse CC-CKR5 prot	AAW54037	19	354	•	776
Human chemokine re	AAW26766	18	332	74.8	839
Macaque chemokine	AAW27125	18	352	•	933
Amino acid sequenc	AAG79089	22	352	•	936
Human G-protein ch	AAU97150	23	352	•	943
Human G-protein ch	AAE07046	22	352	•	943
	AAE07037	22	352	84.0	943
	AAY80128	21	352	•	943
protein	AAW07602	18	352	•	943
Human CCR5 Gln 55	AAM52829	23	352		952
Human CC chemokine	AAW23834	19	371	84.9	953
Fusion protein con	AAY41280	20	439	85.4	958
Human CC chemokine	AAM52828	23	352	85.4	958
Human chemokine (C	ABB08343	23	352	85.4	958
o	AAU97152	23	352	85.4	958
H	AAB46858	22	352	•	958
Human chemokine re	AAE04321	22	352	85.4	958
Human CCR5 protein	AAB83354	22	352	85.4	958
tein	AAE07048	22	352	85.4	958
Human G-protein ch	AAE07039	22	352	85.4	958

ALIGNMENTS

ΡΙΧ	PA	×	PR	PR	XX	ΡF	×	PD	×	PN	×	SO	×	X	X	X	KΨ	X	X	×	DE	×	뎟	×	గై	×	ID AAW	RESULT 1
Libert F, Parmentier M, Samson M, Vassart G;	(EURO-) EUROSCREEN SA.			06-AUG-1996; 96EP-0870102.		28-FEB-1997; 97WO-BE00023.		04-SEP-1997:		WO9732019-A2.		Homo sapiens.		cancer; atherosclerosis; autoimmune disorder.	asthma; idiopathic pulmonary fibrosis; psoriasis; viral infection;	inflammatory disease; rheumatoid arthritis; glomerulonephritis;	predisposition; resistance; diagnosis; treatment; prevention;	human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;	Inactive; human Cys-Cys chemokine receptor 5; CCR5;		Inactive human CCR5.		14-APR-1998 (first entry)		AAW27408;		AAW27408 standard; Protein; 215 AA.	LT 1

N-PSDB; AAT90118

Active and inactive forms of human CC chemokine receptor CCR-5 useful to diagnose, prevent and/or treat inflammatory disorders autoimmune disease and viral infection

disorders,

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AAW88238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
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                29-MAY-1998;
                                                                                                          W09854317-A1
                                                                                                                                                                                Domain
                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIV-1 co-receptor CCR5 variant CCR5-delta32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-MAR-1999
                                                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW88238 standard; Protein; 215 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   idiopathic pulmonary fibrosis and psoriasis, viral infections, especially human immunodeficiency virus type 1 or type 2 (HIV-1 or Subjects that express the inactive receptor have a predisposition,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is an inactive human CC (Cys-Cys) chemokine receptor 5 (CCR5), which lacks the last 3 transmembrane regions and the regions involved in G protein-coupling. CCR5 or its cDNA can used to diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid arthritis, glomerulonephritis, asthma, filesases, e.g. rheumatoid arthritis, glomerulonephritis, asthma filesases, e.g. rheumatoid arthritis, glomerulonephritis, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS
                                                                                                                                                                                                                                                                                                                                                                                                                         CCR5; CCR5-delta32; co-receptor; infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215;
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           98WO-EP03437.
                                                                                                                                                                                                                                                                                                                                                                                                                  human.
                                                                                                                                                                                /note= "transmembrane domain
                                                                                                                                                                                                                    103..124
                                                                                                                                                                                                                               /note= "transmembrane
                                                                                                                                                                                                                                                                                                        Location/Qualifiers 32..56
                                                                                                                                                                                                                                                                     /note= "transmembrane domain 1"
                                                                                                                                                                           . 167
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Pred. No. 1.4e-125;
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domains 5-7. CCRS serves as a co-receptor for infection by macrophage-tropic (M-tropic) strains of HIV-1. Individuals concerning the CCRS-delta32 mutation are resistant to HIV-1. CCRS-delta32 mutation are susceptible. The CCRS-delta32 mutation are resistant of variant CCRS-delta32 mutation who, if infected, may be used to identify CCRS-delta32 mutation who, if infected, may exhibit slower progression to CC diagnostic methods for detecting the presence of such variants. A CC expressing the CCRS-delta32 mutation has provided for inhibiting HIV-1 infection of a cell expressing the CCRS-delta32 mutation has involves introducing a nucleic CC number of functional CCRS-molecules present on the cell surface.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PR XX PA XX PA XX PA XX PA XX XX PA XX XX DR
                       Query Match
Best Local Similarity
              Matches
                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  This is the amino acid sequence of a CCR5 variant protein, designated CCR5-delta32, that includes the first 4 transmembrane domains of wild-type CCR5 (see AAW88232), but lacks transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 38-39; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New CCR5 variant protein of the HIV-1 co-receptor - useful in developing resistance of CCR5-expressing cells to HIV-1 infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arenzana Siesdedos F,
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      Conservative
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                     100.0%;
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      0;
                       Score 1122;
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Mismatches
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                 DB 20;
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                                    Length
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AAW27406
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     Inactive; human Cys-Cys chemokine receptor-5; CCR5; human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2; predisposition; resistance; diagnosis; treatment; prevention; inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma; idiopathic pulmonary fibrosis; psoriasis; viral infection;
cancer; atherosclerosis; autoimmune disorder
                                                                                                                                                                                                                       AAW27406 standard; Protein;
                                                                                                                                                              14-APR-1998
                                                                                                                                                                                               AAW27406;
                                                                                                                         Inactive human CCR5.
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                                                                                                                                                         (first entry)
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121

121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSOKEGLHYTCSS

180 180

LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS

61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

MDYQVSSPTYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR MDYQVSSPIYDINYYTSEBCQKINVKQIAARLLDPLYSLVFIFGFVGNMLVILILINCKR

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LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120

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Matches 184;
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      human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2; dlagnosis; treatment; prevention; inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma; idiopathic pulmonary fibrosis; psoriasis; viral infections.
                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is an inactive human CC (Cys-Cys) chemoking receptor 5 (CCR5), which is not a receptor of human immunodeficiency virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can used to diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid arthritis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis, viral infections, especially HIV-1 or HIV-2 infection, cancer, atheroscierosis and autoimmune disorders. Subjects that express the inactive receptor have a predisposition, or resistance to HIV-1 and/or HIV-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EUKO-) EUROSCREEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MA
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                                                    Human Cys-Cys
                                                                          Human
                                                                                                                                         AAW27407
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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R-1996;
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DB; AAT90116.
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                                                                          CCR5
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atherosclerosis;
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                                                                                                                                                                                                                                                                                                                      standard;
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                                                                                                                                                                                                                                                        LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
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                                                                                                                                                                                                                                                                                                                                                                                                          184 AA;
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ilarity 100.0%;
Conservative
                                                                                              (first
                                                                                                                                                                                                                184
                                                   chemokine receptor 5;
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96EP-0870021
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                                                                                                                                      Protein; 352
                                                                                             entry)
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 autoimmune
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Pred. No.
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                                                    CCR5;
 disorder
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          infection;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                             chemokines, but not by monocyte chemoattractant protein 1 (MCP-1), MCP-3, interleukin-8 (IL-8) or growth related gene product alpha (GRO alpha) chemokines. Active CCR-5 is also a receptor of human immunodefictency virus type 1 or type 2 (HYV-1 or HIV-2). CCR5 or its CDNA can used to diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid arthitis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis, viral infections, especially HIV-1 or HIV-2 infection, cancer, atherosclerosis and autoimmune disorders.
Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour; asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy; diagnosis; leukocyte trafficking;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo
                                                 Human chemokine receptor
                                                                         14-DEC-1997
                                                                                               AAW27123;
                                                                                                                     AAW27123
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Active
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01-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CCR5), which is
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                                                                                                                                                                                                                                                                                                                                                                184;
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                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                   HFPY 184
                                                                                                                                                                                                                                             LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS
                                                                                                                                                                                                                                                                                LKSMTDIYLLNLAISDLFELLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII
                                                                                                                                                                                                                                                                    LKSMTDIYLLNLAISDLEFLLTVPEWAHYAAAQWDEGNTMCQLLTGLYFIGEFSGIFFII
                                                                                                                                                                                                                       LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS
                                                                                                                                                                                                                                                                                                                                                                                                            352 AA;
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                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1b-c;
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96EP-0870021.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e forms of human CC chemokine receptor CCR-5, prevent and/or treat inflammatory disorders, and viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ce is human CC (Cys-Cys) chemokine stimulated by MIP-1 alpha, MIP-1 t
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                                                                                                                    Protein;
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100.0%;
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                                                  88C
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protein coupled

receptor; ligand; modulator; antibody;

human

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Matches
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Best Local :
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                                                                                                                                                                                                                                   88C, a G protein coupled receptor that is involved in leukoyte trafficking. Its amino sequence was deduced from a cDNA clone (AAT85161) isolated from a macrophage library. It shows 628 identity to CCCKRI. Chemokine receptor 88-2B (see AAW27124) has also been identified. 88C and 88-2B receptors and their polypeptide fragments can be produced in transformed host cells. The receptors, peptides comprising one or more of the extracellular or intracellular
                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding chemokine receptors 88-2B and 88C to modulate leukocyte trafficking, e.g. for treatment of inflammation, tumours, viral infections, autoimmune diseases,
                                                                                                                                                                                                                                                                                                            This polypeptide sequence comprises novel 88C, a G protein coupled receptor that is
                                                                                                                                                                                                                                                                                                                                                Claim
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20-DEC-1995;
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DB; AAT85161.
                                                                                                 184;
      61
                                                                                                                                                                                                                                                                                                                                               16; Page 47-48;
                                            Similarity
LKSMTDIYLLNLAISDLEFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII
             LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCOLLTGLYFIGFFSGIFFII 120
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                                                                                                                                               352
                                                                                               Conservative
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95US-0575967
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259..280
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               Claim 68; Fig 1C; 70pp; English
                                                               WPI; 1998-032650/03.
N-PSDB; AAT76920.
                                                                                           Feng
                                                                                                     Alkhatib
                                                                                                                                          28-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                          Domain
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                                  chemokine receptor 5 polypeptide - sion between HIV and a target cell
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                                                                                          G, Berger Kennedy PE,
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                                                                                                                       HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers 29..55
                                                                                                                                                                                                                  /note= "transmembrane domain'
                                                                                                                                                                                                                              'label=
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                                                                                                                                                                                                                                                                                                                                                              /note= "transmembrane
143..171
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                                                                                           EA, Broder CC,
, Murphy PM;
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                                                                                                                                                                                                                                                                                                                        "extracellular loop-2 (Claim 19)"
                                                                                                                                                                                                                                               "extracellular
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                                                                                                                                                                                                                                                                                                        This invention describes a novel receptor polypeptide (I) selected from (I) a fully defined 329 amino acid sequence (II) fully disclosed in the specification; and (II) a polypeptide encoded by the cDNA contained in a CC plasmid, and fragments, analogs and derivatives of the polypeptide. The CC products of the invention have antificiammatory, immunomodulatory, CC anticoagulant, antiallergic, immunosuppressive, vulnerary, cytostatic, CC antiparasitic, antipacriatic, antirheumatic, antiarthritic and vasotropic activity and can be used for gene therapy. The G-protein chemokine CC activity and can be used for gene therapy. The G-protein chemokine CC activate or inhibit activation of (I). The products of the invention can also be used for stimulating hacmatopolesis, wound healing, coagulation, CC anglogenesis, treating solid tumours, chronic infections, leukemia, CC Tcell mediated autoimmune diseases, parasitic infections, psoriasis, and CC allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation, histamine and immunoglobulin E (IGE)-mediated allergic calcions, prostaglandin-independent fever, bone marrow failure, CC silicosis, sarcoidosis, rhoumatoid arthritis, shock and
                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUN-1995;
18-NOV-1998;
25-JUN-1999;
                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human G-protein chemokine receptor polypeptides and polypucleotides, useful for identifying (ant)agonists to the G-protein chemokine receptor -
                                                                                                                                                                                                                                                                                                                                                       hyper-eosinophilic syndrome. (N.B. This record was resubm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-226317/23
N-PSDB; AAF26390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T-ccll mediated autoimmune disease; psoriasis; allergy; atherogenesis; anaphylaxis; malignancy; inflammation; histamine; IgE; silicosis; shock; immunoglobulin E-mediated allergic reaction; rheumatoid arthritis; prostaglandin-independent fever; bone marrow failure; sarcoidosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L1 Y,
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(RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-NOV-2000; 2000US-0725285
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                                              LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                                                                                          LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
                            LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS
                                                                                                                                                                                                                                                                                                     352 AA;
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98US-0195662.
99US-0339912.
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                                                                                                                                                                                                                                                                                                                                                   to correct errors in the keyword
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Search completed: June Job time: 40.4356 secs ω

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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents the human CCR5 protein sequence. The invention relates to a method for determining whether an agent is capable of modulating the interaction of chemotactic chemokine receptor (CCR5) with 9p120, comprising incubating the agent with CCR5 and 9p120 and determining whether the agent modulates the interaction, where 9p120 is associated with CD4, and where the interaction is a low affinity binding. The method is used to identify an agent capable of modulating the interaction of CCR5 with 9p120. An agent identified by the method is used to prepare a pharmaceutical composition for the treatment of a disease or condition associated with CCR5 and 9p120 interaction, to treat a subject with a disease or condition associated with CCR5 and 9p120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interaction, and for preparing a pharmaceutical for treating human immunodefictency virus (HIV). It can also be treat anti-inflammatory diseases. The method is commercially useful, amenable to high throughput screening, and detects interaction of gp120 with cells expressing only
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                                                                                                                                                                                                                                                                     Human; transformed mammalian cell; CD4; reporter gene; translocation; human immuno deficiency virus; HIV; long terminal repeat; LTR; therap; chemokine receptor; CKR; cellular dysfunction; HIV infection; cofacto CC-CKR-5; envelope glycoprotein; anti-HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 110; 113pp;
20-MAY-1996;
                                                   21-MAY-1997;
                                                                                                                                                               US6258527-B1
                                                                                                                                                                                                                                                                                                                                                                                                           Human chemokine receptor (CKR), CC-CKR-5 related
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DB; AAF87099.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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     96US-0017157
                                                      97US-0861105
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100.0%;
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Pred. No.
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RESULT 15 AAB46858

AAB46858 standard; Protein;

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AAB46858;

Human HDGNR10 protein.

HDGNR10; human; G-protein chemokine receptor; antiinflammatory; immunomodulatory; anticoagulant; antiallergic; immunosuppressive; cytostatic; antiparasitic; antipsoriatic; antirhumatic; antiarhittic; vasotropic; gene therapy; haematopoiesis; wound healing; coagulation; angiogenesis; solid tumour; infection; leukemia; growth factor activity

activity;

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Best Local S
Matches 184
                                                                                                                                                                                                                                                                                                   the cell surface of transformed mammalian cell. The invention is useful for identifying drugs or antibodies that interfere with the translocation of HIV into transformed mammalian cell or for identifying a human chemokine receptor that facilitates the infection of a particular HIV strain into the transformed mammalian cell. Compounds identified can be used to treat cellular dysfunction and to prevent or combat HIV infection. The present sequence is a human chemokine receptor (CKR), CC-CKR-5 related protein. CC-CKR-5 is the principal cofactor for entry mediated by the envelope glycoproteins of primary macrophage-tropic
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human c
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(UYNY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
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19-MAY-1997;
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181
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                                                                                                                                                                                                                                                                                                                                                                                                                                  t (LTR) and that has been transduced with a vector encoding a chemokine receptor (CKR) where the CD4 and the CKR are present
                                                                                                                                                                                                     184;
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                                             LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLFGIIFTRSQKEGLHYTCSS
                                                                                                     LKSMTDIYLLNLAISDLEELLTVPFWAHYAAAQWDEGNTMCQLLTGLYEIGEESGIFEII
                                                                                                                                                          MDYQVSSPIYDINYYTSBPCQKINYKQIAARLLPPLYSLYFIFGFVGNMLVILILINCKR
   HFPY 184
                                                                                      LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII
                                                                                                                                              MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR
                              LITIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS
                                                                                                                                                                                                                                                             352 AA;
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                                                                                                                                                                                                     Conservative
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97US-0858660.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a construct encoding a reporter muno deficiency virus (HIV) long
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or treatment of
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              The invention relates to human G-protein chemokine receptor HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antib are useful for treating, preventing or ameliorating a diseas
                                                                                                                                                                                                                                       09-FEB-2000; 2000US-0181258.
09-MAR-2000; 2000US-0187999.
22-SEP-2000; 2000US-0234336.
                                                                                             Isolated nucleic acid encoding a human G-protein chemokine receptor (CCRS) HIGNRIO polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
                                                                                                                                                                                                                                                                                                                                                                                 Human; G-protein chemokine receptor; CCRS; HDGNR10; inflammation; HIV; human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; cytostatic; immunosuppressive; noctropic; neuroprotective; gene therapy; nourodegenerative disorder; Kaposi's sarcoms; autoimmune disease; rhoumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; pastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia.
                                                                                                                                                                                            Rosen CA,
                                                                                                                                                                                                                                                                                       09-FEB-2001; 2001WO-US04153
                                                                                                                                                                                                                                                                                                                    16-AUG-2001
                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                           WO200158916-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human G-protein chemokine receptor (CCR5) HDGNR10 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE07048 standard;
                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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DB; AAD13299.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HFPY 184
                                                                  Page
                                                                                         neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                504-505; 518pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein; 352
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enting or ameliorating a disease or disorder defective or aberrant chemotaxis of immune
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's CC sarcoma) or defective or aberrant T-cell antigen presenting cell CC interaction. The disease or disorder may also be an infectious disease CC (e.g. a viral infection, such as an early stage HIV infection, a CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The CC disease or disorder may be associated with aberrant CCR5 expression, lack CC function. CCR5 HDGNR10 protein is used as a food additive or preservative CC function. CCR5 HDGNR10 protein and in gene therapy. CCR5 HDGNR10 DNA are useful CC protein, antibodies, agonists and antagonists are also useful in the CC disposis, treatment and prevention of cancer (breast, ovary, adrenal CC urogenital); immune disorders (Addison's disease, allergies, autoimmune CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular disorders (myocardial ischaemias) and colitis); cardiovascular disorders (myocardial ischaemias) and colitis); cardiovascular disorders (myocardial ischaemias) and county protein. The present sequence is human CCR5 HDGNR10 protein.
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                                                                     12-JAN-2000;
12-JAN-2000;
12-JAN-2000;
                               (PFIZ )
                                                                                                                     03-JAN-2001; 2001EP-0300020
                                                                                                                                                                                                              Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5; human immunodeficiency virus; anti-inflammatory disease; human.
                                                                                                                                                                        EP1118858-A2
                                                                                                                                                                                                                                                       Human CCR5 protein sequence
                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                       09-OCT-2001
                                                                                                                                                                                                                                                                                                                                    AAB83354 standard; Protein; 352
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PFIZER
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       Perros M,
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ilarity 100.0%;
Conservative (
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      Rickett GA;
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Pred. No. le-105;
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181 HFPY 184

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The present sequence is that of human HIV-1 co-receptor CCR5.

CC Amino acids 2-18 in the N-terminal region of CCR5 comprise an HIV-1 CC gp120-binding site that determines the specificity of the CC interaction between CCR5 and HIV-1 gp120. Post-translational CC sulfation of the tyrosine residues in the CCR5 N-terminus is CC susceptibility of target cells to HIV-1 infection in vivo. The CCC susceptibility of target cells to HIV-1 infection in vivo. The CCC are based on the CCR5 N-terminal region and which are effective CC for inhibiting HIV-1 binding to CCR5. These peptides are used in CC claimed methods of inhibiting HIV infection of CD4+ cells, of C1 claimed methods of inhibiting HIV infection of CD4+ cells, of CCR5 receptor. The methods may be carried out in a subject whose CD4+ cells are infected with HIV, and of cCR5 receptor. The methods may be carried out in a subject which inhibits binding of a CCR5 ligand to a CCR5 receptor. The methods may be carried out in a subject which inhibits binding of a CCR5 ligand to a cCR5 receptor. The methods may be carried out in a subject who is not infected with HIV (prophylactic method), or in a subject who is not infected to with, but has been exposed to, HIV.
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HIV-1; infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 30; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel compounds comprising specific amino acids within CCR5 (HIV 1 co-receptor) amino terminal domain including negatively charged an sulfated tyrosine residues is useful for treating HIV infection in
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)B; AAH26903.
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                                                                                                                                                                                                  Similarity
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                       HFPY 184
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; 2000US-205839P.
; 2001US-267231P.
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2..18
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; therapy; vaccine;
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                                                                                                                                                                                                                 85.4%;
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                                                                                                                                                                                                   Score 958; Pred. No.
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anti-HIV-1.
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AAE07039
ID AAT
AAE07039 standard; Protein; 352 AA
                                                                                                                                                                       Human G-protein chemokine receptor (CCR5) HDGNR10 protein
                                                                                                                                                                 Human;
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                                                                                                                                                                                  AAE07039
                                                                                                                                                                 G-protein chemokine receptor; CCR5; HDGNR10;
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rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; disetes mellitus; allergy; multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia. human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; cytostatic; immunosuppressive; nootropic; neuroprotective; gene ther neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease; inflammation; gene therapy;

Homo sapiens.

09-FEB-2000; 2000US-0181258. 09-MAR-2000; 2000US-0187999. 22-SEP-2000; 2000US-0234336. WPI; 09-FEB-2001; 16-AUG-2001. WO200158915-A2 Rosen N-PSDB; AAD13198 (HUMA-) HUMAN GENOME SCI INC 2001-488965/53 Ç, Roschke V, 2001WO-US04152 Ľ ۲, Ruben X

Isolated nucleic acid encoding a human G-protein chemokine receptor (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders -

Example 40; Page 486-487; 495pp; English

CC protein. CCR5 HDGNRIO antibodies are useful for treating, preventing a disease or disorder associated with inflammation, CCC or ameliorating a disease or disorder associated with inflammation, CCC defective or aberrant chemotaxis of immune cells, HIV infection (such as CC aberrant T-cell antigen presenting cell interaction. The disease or CC aberrant T-cell antigen presenting cell interaction. The disease or CC as an early stage HIV infection, a cytomegalovirus infection such CC an enurodegenerative disorder. The disease (e.g. a viral infection such CC an enurodegenerative disorder. The disease or disorder may be associated CC with aberrant CCR5 expression, lack of CCR5 incation, aberrant CCR5 (with aberrant CCR5 axpression, lack of CCR5 incation, aberrant CCR5 (company) and company c The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10 protein. CCR5 HDGNR10 antibodies are useful for treating, preventing

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Best Local Similarity
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       Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection; inflammation; autoimmune disease; metastasis; bronchial asthma; lupus; chronic bowel inflammation; rheumatoid arthritis; cytostatic; antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
     antirheumatic; antiarthritic
                                                                          Human CCR5
                                                                                               17-JAN-2002
                                                                                                                                        AAG80111 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to G protein-coupled receptors (GPCRs) for whithe endogenous ligand has been identified. Non-endogenous constitutively activated versions of known GPCRs are used in the invention for the direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists. Such agonists are useful as therapeutic agents for diseases or disorders associated with GPCRs. The present sequence is a non-endogenous version of a known human GPCR.
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Synthetic.
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DB; ABI97978.
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              394pp; English.
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Pred. No. 1e-105;
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Best Local :
                            AAB82948;
    21-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                             or prostatic), organ rejection, inflammation and autoimmune diseases. Also inhibitors of (I) are used therapeutically against tumors (and their inflammation), or autoimmune diseases (rheumation) are autoimmune diseases (rheumation) are autoimmune diseases (rheumation) are autoimmune diseases (rheumation) are chronic bowel where the (cardio)vascular, lymphatic, respiratory, narvous, diseastive, endocrine, motor or urogenital systems or skin are affected, and bone which have cytostatic, antiinflammatory, antiasthmatic, which have cytostatic, antiinflammatory, antiasthmatic, chemokines act on specific tumor and inflammatory cells through a constellation of chemokine receptors (CR), which control migration and proliferation of these cells. AAG80045-AAG80128 represent human chemokine fragments used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diagnostic agent containing two or more receptor-specific ligands, useful for detecting tumors, inflammation etc., also therapeutic use ligand inhibitors
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Pred. No.
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of.

Human HIV-1 co-receptor CCR5

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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC chemokine receptor that has been designated CCR5. The sequence was deduced from an isolated cDNA clone (see AAT76920). An Ala177Leu variant (see W238340 of CCR5 was also identified. The susceptibility cof human macrophages to HIV infection depends on cell surface expression of CD4 and CCR5. CCR5 is a member of the 7-transmembrane capperfamily of G-protein coupled cell surface molecules. It plays can essential role in the membrane fusion step of infection by some CRT visolates. The establishment of stable, non-human cell lines and transgenic mammals having cells that coexpress human CD4 and CCR5 provides valuable tools for research of HIV infection. CRS provides valuable tools for research of HIV infection. CRS capable of blocking membrane fusion between HIV and target cells represent potential anti-HIV therapeutics for macrophage
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84; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            352 AA;
                                                                                                                                                                                                                                                   CCR5m303; co-receptor;
                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                         human.
                                                                                                                                                                  /note= "transmembrane domain 1"
67..87
                                                                                                                                               /note= "transmembrane domain 2"
101
                                                                                                                                                                                      Location/Qualifiers 32..56
                               /note=
275..3
                                                                                                                 103..124
                                                                                                                          /note= "corresponds to TGT (Cys) in wild-type CCR5 TGA (Stop) in CCr5m303"
                                                     236...260
                                                                         200:.223
                                                                                              142..167
                                                                                                       /note=
                                                               'note=
                                                                                  note-
                                                                                                     "transmembrane domain 3"
                                                                                    "transmembrane
                                           "transmembrane
                                                               "transmembrane
                     *transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 958; DB 19;
Pred. No. 1e-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                      infection; diagnosis; AIDS;
                                           domain 6"
                                                                 domain
                                                                                     domain 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                           7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
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Huma
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                                                                                                                                                                                                                                                                                                                                                                                                                         ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This is the amino acid sequence of wild-type human CCR5, which correceptor for infection by macrophage-tropic (M-tropic) strains of HIV-1. The invention relates to the CM-tropic) strains of HIV-1. The invention relates to the invention relates to the CM-tropic) strains of HIV-1. The invention relates to the comprising the first two transmembrane domains of wild-type CCR5, comprising the first two transmembrane domains of wild-type CCR5, comprising the first two transmembrane domains of wild-type CCR5, comprising the first two transmembrane domains of wild-type CCR5, comprising the many indicate shows a positive correlation with respice HIV-1 correlation with respication of the disease. The CM-trains, and may indicate slower progression of the disease. The converted, and the properties of the disease of the converted, may exhibit slower progression to AIDS. Probes and infected, may exhibit slower progression to AIDS. Probes and converted the presence of such variants. A method is provided for inhibiting HIV-1 infection of a cell expressing the CCR5 creek converted to the cell, thereby reducing a nucleic acid encoding a CCR5 correction.
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                                                                                                                                                                    RESULT 8
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Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-059835/05.
N-PSDB; AAV84126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arenzana Siesdedos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOND-) FOND MONDIALE RECH & PREVENTION SIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New CCR5 variant protein of the HIV-1 co-receptor - useful in developing resistance of CCR5-expressing cells to HIV-1 infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 34-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
Human; G protein-coupled receptor; GPCR; non-endogenous;
constitutively activated GPCR; agonist; disease.
                                            Non-endogenous human GPCR protein,
                                                                          18-FEB-2002
                                                                                                          ABB56342
                                                                                                                                    ABB56342 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              molecules present on the cell surface.
                                                                                                                                                                                                                                               181
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                                                                                                                                                                                                               HFPY 184
                                                                                                                                                                                                                                                                           LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS
                                                                                                                                                                                                                                               HFPY 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0048057.
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                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.4%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 958;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ۶
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                   SEQ ID NO: 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1e-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quillent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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120

60

120

180

OM protein protein search, using sw model

Run on: June 3, 2003, 15:16:36; Search time 19.7178 Seconds (without alignments)
1048.235 Million cell upda:

cell updates/sec

Title: Perfect score: US-09-939-226-6 1122

MDYQVSSPIYDINYYTSEPC..

.AACHGHLLLGNPKNSASVSK 215

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Scarched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB Maximum DB seq length: 0
scq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 100 Listing first 45 summaries

Database : prR_73:* 1: pir1:* pir2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score 958	5 : 66	Length	, N B	ID A43113	်ဂို မြိ
ωı	694	61.9	374	د د	138450	chemokine (C-C)
^	598	u	355	ພ	A45177	ر م
տ	573.5	-	355	N	149339	e in
6	547.5	48.8	360	N	A57160	(0-0)
7	546.5	•	360	N	JC4587	<u>۾</u>
80	535.5	47.7	359	ພ	149341	-
9	506.5	•	355	N	G02436	kine (c-c)
10	489.5	43.6	356	ພ	I49340	MIP-1 alpha recep
=	449	•	383	ผ	S55594	0
12	427.5	38.1	355	ผ	JC5067	G protein-couple
13	386	34.4	354	N	158186	probable G protein
14	378	•	344	N	JC5942	chemokine receptor
15	365	32.5	355	ผ	JC4304	ס
16	345.5	•	378	N	B55735	ž
17	342.5	٠	378	N	A55735	G protein-coupled
10	333.5	•	378	N	A45680	G protein-coupled
19	331.5	٠	352	ພ	A45747	
20	326	•	353	ພ	S28787	neuropeptide Y/pep
21		•	352	ພ	G00048	₹
22	321.5	•	359	ພ	151372	angiotensin II rec
23	320		369	ນ	JC5068	胆
24	317	•	359	ມ	JC1194	angiotensin II rec
25	314	٠	359	ພ	A42656	II
26	312	•	359	N	JC1104	H
27	312		359	ພ	139418	
28	311		359	,	TC2134	H
၁	310					angiotensin II rec

5	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	
265	267	269	270.5	273.5	274.5	276	276	276	283	287.5	291	306	307	308	309	
23.6	23.8	24.0	24.1	24.4	24.5	24.6	24.6	24.6	25.2	25.6	25.9	27.3	27.4	27.5	27.5	
355	363	360	388	384	359	364	363	333	362	367	350	359	359	359	359	
N	N	Ň	N	N	N	ນ	Ν	N	N	N	N	N	N	N	N	
JQ1231	I57940	A53611	JN0605	A47249	A48921	JN0763	I57955	I65989	JN0694	JE0349	JN0621	JQ1516	S44425	A48857	JH0621	
interleukin-8 rece	somatostatin recep	interleukin-8 rece	somatostatin recep	brain-specific som	interleukin-8 rece	somatostatin recep	somatostatin recep	G protein-coupled	angiotensin II rec	interferon-inducib	G protein-coupled	angiotensin II rec	angiotensin II rec	angiotensin II rec	angiotensin II rec	

ALIGNMENTS

emokine (C-C) receptor 5 - human Alternate names: C-C CRR-5; CCR5 Alternate names: C-C CRR-5; CCR5 Species: Homo saptens (man) Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 20-Jun-2000 Date: 12-Jul-1996 #text_change 20-Jun-2000 Date: 12-Jul-1996 #sequence_revision Assession of a new human CC-chemokine receptive: Molecular cloning and functional expression of a new human CC-chemokine receptive: Molecular cloning and functional expression of a new human CC-chemokine receptive: Molecular cloning and functional expression of a new human CC-chemokine receptive:

A; Molecule type: mRNA A; Residues: 1-352 <SAM1> Reference number: A43113; MUID:96241590; PMID:8639485

A;Cross-references: GB:X91492; NID:g1262810; PIDN:CAA62796.1; PID:g1262811 R;Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Sarag M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Nature 382, 722-725, 1996

A;Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant allele A;Reference number: S71808; MUID:96345670; PMID:8751444 A; Accession: S71808

Status: nucleic acid sequence not shown; not compared with conceptual translation

A; Molecule type: DNA
A; Residues: 182-206; 207-230 <SAM2>
A; Accession: A58834 Status: nucleic acid sequence not shown; not compared with conceptual translation

A; Molecule type: DNA
A; Residues: 1-184, 'IRDSHLGAGPAAACHGHLLLGNPKNSASVSK' <SAM3>
A; Residues: 1-184, 'IRDSHLGAGPAAACHGHLLLGNPKNSASVSK' <SAM3>
A; Cross-references: GB: X99393; NID: g1524062; PIDN: CAA67767.1; PID: g1524063
A; Note: this frameshift mutation results in a non-functional receptor but confers nd may have had a selective advantage by conferring resistance to Yersinia plague R; Combaddiere, C: Anuja, S.K.; Tiffany, H.L.; Murphy, P.M.

inf

J. Leukoc. Biol. 60, 147-152, 1996 A;Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine A:Reference number: A58832; MUID:96295970; PMID:8699119

A; Accession: A58832

A;Accession.A;Accession. A;Accession. A;Accession. A;Accession. A;Accession. A;Accession. A;Residues: 1-352 <COM1>
A;Residues: 1-352 <COM1>
A;Cross-references: GB:U57840; NID:g1502408; PIDN:AAB17071.1; PID:g1502409
A;Cross-references: GB:U57840; PID

R;Combadiere, C. submitted to the EMBL Data Library, May 1996 A:Reference number: H01541 A; Reference number: A; Accession: G02653

A;Status: translated from GB/EMBL/DDBJ

A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-89, 'L', 91-352 <COM2>
A; Cross-references: EMBL:U57840
A; Cross-references: EMBL:U57840
R; Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
J. Biol. Chem. 271, 17161-17166, 1996
J. Biol. Chem. 271, 17161-17166, 1996
A; Title: Molecular cloning and functional characterization of a novel human CC chemok
A; Reference number: A58833; MUID:96291862; PMID:8663314

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A;Accession: A58834
A;Accession: A58834
A;Kolecule type: mRNA
A;Kolecule type: mRNA
A;Kolecule type: mRNA
A;Kolecule type: mRNA
C;Coss references: GB:U54994; NID:g1457945; PIDN:AAC50598.1; PID:g1457946
A;Cross references: GB:U54994; NID:g1457945; PIDN:AAC50598.1; PID:g1457946
C;Comment: This is a receptor for chemokines MIP-lalpha (see PIR:A30574), MIP-lbeta (se
                                                                                                                          A;Cross-references: DDB:D29984; NID:g531246; PIDN:BAA06253.1; PID:g531247 R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughli Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994 A;Title: Molecular cloning and functional expression of two monocyte chemoa A;Reference number: A53477; MUID:94195821; PMID:8146186 A;Accession: I38463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Date: :
C; Access:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N;Alternate names: C-C CKR-2; monocyte cC;Species: Homo ganion- /--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 3p21-3p21
C;Function:
A;Description: G protein-coupled receptor for chemokines MIP-lalpha, MIP-lbeta
A;Note: probably acts to control granulocyte proliferation and differentiation
C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                  R;Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N. Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
A;Title: cDNA cloning and functional expression of a human monocyte A;Reference number: JC2443; MUID:94324942; PMID:8048929
A;Accession: JC2443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;103-124/Domain: transmembrane #status predicted <TM3> F;142-166/Domain: transmembrane #status predicted <TM4> F;143-218/Domain: transmembrane #status predicted <TM5> F;133-218/Domain: transmembrane #status predicted <TM5> F;236-257/Domain: transmembrane #status predicted <TM6> F;285-300/Domain: transmembrane #status predicted <TM7> F;20-269,101-178/Disulfide bonds: #status predicted
  A; Cross-references:
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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                                                                             A; Molecule type: mRNA
                                                                                                  A; Status: preliminary
                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-360 < YAM>
                                                       A;Residues: 1-360 <RES>
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268/Binding site: carbohydrate (Asn) (covalent) #status predicted 336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted 340,343/Binding site: phosphate (Thr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-Feb-1995 #sequence_revision 05-Apr-1995 ion: JC2443; I38463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 HFPY 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 LKSMTDIYLLNLAISDLEFLLTVPFWAHYAAAQWDEGNTMCQLLTGLYFIGEFSGIFFII 120
61 LKSMTDIYLLNLAISDLEFLLTVPFWAHYAAAQWDEGNTMCQLLTGLYFIGEFSGIFFII 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLTIDRYLAVVHAVEALKARTVTFGVVTSVITWVVAVEASLPGIIFTRSQKEGLHYTCSS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                             EMBL: U03905; NID: 9472557; PIDN: AAA19120.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDB:1230510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.4%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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OMIM:601373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 958;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.2e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phosphoprotein; transmembra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      predicted
                          PID:g472558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-Jun-2000
                                                                                                                                                                                                                               Coughlin,
                                                                                                                                                                                                                                                                                                                                                                                          chemoattractant
                                                                                                                                                                                  chemoattractant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               monocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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A; Map position: 3p21-3p21
c) Superfamily: vertebrate rhodopsin
c) Superfamily: vertebrate rhodopsin
c) Keywords: alternative splicing; G protein-coupled receptor;
c; Keywords: alternative splicing; G protein-coupled receptor;
c; 43-70/Domain: transmembrane #status predicted <TM1>
c; 81-100/Domain: transmembrane #status predicted <TM2>
c; 81-100/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                     F;244-265/Domain: transmembrane #status predicted <TM6>F;292-309/Domain: transmembrane #status predicted <TM7>F;14/Binding site: carbohydrate (Asn) (covalent) #status F;32-277,113-190/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                     F;115-136/Domain: transmembrane #status predicted <TM3>F;154-178/Domain: transmembrane #status predicted <TM4>F;208-226/Domain: transmembrane #status predicted <TM5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Keywords: alternative splicing; G protein-coupled receptor;
F;44-68/Domain: transmembrane #status predicted <TM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GDB:337364; OMIM:601267
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A;Title: Molecular cloning and functional expression of two monocyte chemoatts A; Reference number: A53477; MUID:94195821; PMID:8146186
A; Accession: I38450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: GDB:CMKBR2
A;Cross-references
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;44-68/Domain: transmembrane #status predicted F;79-99/Domain: transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-374 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chemokine (C-C) receptor 2, splice form A -
N;Alternate names: C-C CKR-2; monocyte chemo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:U03882; NID:g472555; PIDN:AAA19119.1; PID:g472556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: I38450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             I38450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
        Matches
                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: GDB:337364; OMIM:601267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                           61.9%;
75.9%;
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Score 694; DB 2;
Pred. No. 2.5e-56;
7; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 694; DB 2; 1
Pred. No. 2.4e-56;
7; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-Feb-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chemoattractant protein 1 receptor; monocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ^TM2>
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                                                                              Length 374;
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                                                                                                                                                                                                            predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glycoprotein;
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    2
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    Gaps
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10

YDINYYTSEPCQKINYKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYL

81

FDYDY--GAPCHKFDYKQIGAQLLPPLYSLYFIFGFYGNMLYYLILINCKKLKCLTDIYL LNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLA

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N;Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999 C;Accession: A45177; I55671 R;Neoto, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: GDB:CMKBR1; CMKR-1
A;Cross-references: GDB:138446; OMIM:601159
A;Map position: 3p21-3p21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molocule type: mRNA
A;Residues: 1-355 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Molecular cloning,
A;Reference number: A45177,
A;Accession: A45177
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C;Roywords: disulfide bond; G protein-coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Structure and functional expression of the human macrophage inflammatory 1 alpla; Reference number: I55671; MUID:93240122; PMID:7683036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; A;Experimental source: HL60 cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . Exp. Med. 177, 1421-1427, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240-264/Domain: transmembrane #status predicted <TM6>
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                            345/Binding site: phosphate (Ser) (covalent) (by casein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                  5/Binding site: carbohydrate (Asn) (covalent) #status predicted 24-273,106-183/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36-60/Domain: transmembrane #status predicted <TM1>71-91/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence extracted from NCBI backbone (NCBIP:124876)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; 415-425, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (C-C) receptor 1 - human
                                        181
                                                                                  126
                                                                                                                             121
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                                                                                                                                                                                                                                                  HFPY 184
                                                                                                                         LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS
                                                                                                                                                                   KNWTSTYLLNLAISDLLFLFTLPFWIDYKLKDDWVFGDAMCKILSGFYYTGLYSEIFFII
                                                                                                                                                                                          KSMTDIYLLNLAISDLFFLLTVPFWAHYAAA-QWDFGNTMCQLLTGLYFIGFFSGIFFII 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLTIDRYLAIVHAVFALRARTVTFGVITSIIIWALAILASMPGLYFSKTQWEFTHHTCSL
                                                                                                                                                                                                                                                                                                                                           Conservative
189
                                                                                                                                                                                                                                                                                                                                       53.3%; Score 598; DB 2; L
59.2%; Pred. No. 1.6e-47;
59.2%; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          functional expression, and signaling characteristics of a MUID:93161416; PMID:7679328
                                                                                                                                                                                                                                                                                                                                                                                 Length 355;
                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glycoprotein; phosphoprotein;
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                                                                                . 185
                                                                                                                                                                                                                                                      65
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Query Match

/Binding site: phosphate (Thr) (covalent) (by protein kinase

Best Local Similarity Matches 100; Conserv

Conservative

36;

Mismatches ŏ .

48.8%;

Pred.

.1e-43;

DB 2;

Length Indels

360;

C

#Status

predicto

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Gaps

<u>ب</u>

Score 547.5;

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macrophage inflammatory protein-1 alpha receptor - mouse C;Species: Mus musculus (house mouse) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999 C;Accession: I49339 R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three mouse A;Reference number: I49339; MUID:95340546; PMID:7542241
A;Accession: I49339
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A. Map position: 3p21-3p21

C; Superfamily: vertebrate rhodopsin

F; 40-65/Domain: transmembrane #status predicted <TM1>
F; 6-97/Domain: transmembrane #status predicted <TM4>
F; 111-133/Domain: transmembrane #status predicted <TM5>
F; 211-175/Domain: transmembrane #status predicted <TM6-
F; 243-264/Domain: transmembrane #status predicted <TM6-
F; 243-264/Domain: transmembrane #status predicted <TM7-
F; 29-276,110-187/Disulfide bonds: #status predicted
F; 72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase C) #status predicte
F; 145/Binding site: phosphate (Ser) (covalent) (covalent) #status predicted
F; 183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A; Title: Molecular cloning and functional expression of a novel CC chemokine re A; Reference number: A57160; MUID:95370289; PMID:7642634
A; Accession: A57160
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C;Species: Homo sapiens (man)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C;Accession: A57160
C;Accession: A57160
C;Accession: A57160
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A; Residues: 1-360 < POW>
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A; Residues: 1-355 < RES>
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A; Gene: cc ckr-4
C; Superfamily: ve
C; Keywords: glyco
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C;Species:
C;Date: 08
C;Accessio
                                                                        A; Reference number: A; Accession: I49341
                                                                                                                     R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501,
A;Title: Cloning and differential
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149341
A; Molecule a
A; Residues:
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A;Experimental source: thymus
C;Genetics:
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A;Molecule type: mRNA A;Residues: 1-360 <HOO>
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                                                                                                                                                                                                                ;Species: Mus musculus (house mouse);Date: 02-Jul-1996 #sequence_revision
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|Species: Mus musculus (house mouse)
|Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change
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55.98;
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MUID:95340546; PMID:7542241
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C;Species: H
C;Date: 21-D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: H01272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C: Keywords: G protein-coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GDB: 579624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: GDB: CMKBR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: G02436;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Species: Homo sapiens (man);Date: 21-Dec-1996 #sequence_revision;Accession: G02436; A57237
                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                            345/Binding site:
                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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                                                                                                                                                                                                                                         Similarity
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                 LVTLPFWIHYVRGHNWVFGHGMCKLLSGFYHTGLYSEIFFIILLTIDRYLAIVHAVFALR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor 3
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57.6%;
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57.9%;
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A; Survey : mRNA
A; Molecule type: mRNA
A; Residues: 1-106,'N',108-275,'S',277-280,'R',282-355 <COM>
A; Residues: 1-106,'N',108-275,'S',277-280,'R',282-355 <COM>
A; Residues: 1-106,'N',108-275,'S',277-280,'R',282-355 <COM>
A; Residues: 1-106, Note: 1-106, Note: the translated sequence in GenBank entry HSU28694, release 113.0, Note: the translated sequence in GenBank entry HSU28694, release 113.0, Note: the translated sequence in GenBank entry HSU28694, release 113.0, Note: the translated sequence in GenBank entry HSU28694, release 113.0, Note: the translated sequence in GenBank entry HSU28694, release 113.0, Note: the translated sequence in GenBank entry HSU28694, release 113.0, Note: the translated sequence in GenBank entry HSU28694, Note: the translated sequence in GenBank entry HSU28694, release 113.0, Note: the translated sequence in GenBank entry HSU28694, release 113.0, Note: the translated sequence in GenBank entry HSU28694, Note: the translated sequence in GenBank entry HSU28694, release 113.0, Note: the translated sequence in GenBank entry HSU28694, release 113.0, Note: the translated sequence in GenBank entry HSU28694, release 113.0, Note: the translated sequence in GenBank entry HSU28694, release 113.0, Note: the translated sequence in GenBank entry HSU28694, release 113.0, Note: the translated sequence in GenBank entry HSU28694, release 113.0, Note: the translated sequence in GenBank entry HSU28694, release 113.0, Note: the translated sequence in GenBank entry HSU28694, NOTE: the translated seque
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R;Combadiere, C.; Ahuja, S.K.; Murphy, P.M.
J; BiOl: Chem. 270, 16491-16494, 1995
A;Title: Cloning and functional expression of a human ed
A;Reference number: A57237; MUID:95348056; PMID:7622448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;288-305/Domain: transmembrane #status predicted <TM7> F;24-273,106-183/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   r;14/-1/1/Domain: transmembrane #status predicted <TM4>
F;205-223/Domain: transmembrane #status predicted <TM5>
F;240-261/Domain: transmembrane #status predicted <TM6>
F;240-261/Domain: transmembrane #status predicted <TM6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Keywords: G protein-coupled receptor; glycopro
F;36-60/Domain: transmembrane #status predicted
F;71-91/Domain: transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;108-129/Domain: transmembrane #status predicted <TM3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: nucleic acid sequence not shown
                                                                                                                                                                                LLTVPFWAHYAAA-QWDFGNIMCQLLIGLYEIGFFSGIFFIILLTIDRYLAVVHAVFALK: 138
                                                                                                                                  CEKADTRALMAQFVPPLYSLVFTVGLLGNVVVVMILIKYRRLRIMTNIYLLNLAISDLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVFALKARTVIFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYLLNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVFALRARTVTFATITSIITWGLAGLAALPEFIFHESQDSFGEFSCSPRYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISDLFELLTVPFWAHYAA-AQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLAVVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISDLLFLFTVPFWIHYVLWNEWGFGHYMCKMLSGFYYLALYSEIFFIILLTIDRYLAIVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YEWAPPCEKVRIKELGSWLLPPLYSLVFIIGLLGNMMVVLILIKYRKLQIMTNIYLFNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OMIM: 601268
                                                                                                                                                                                                                                                                                                         Score 506.5; DB 2;
Pred. No. 4.2e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 535.5; DB Pred. No. 9e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (covalent)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (by casein kinase II)
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                                                                                                                                  83
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RESULT 11

$55594

$57594

SPOTCEIN-coupled receptor E1 - equine herpesvirus 2

C;Species: equine herpesvirus 2

C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999

C;Accession: $55594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R:Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A:Title: Cloning and differential tissue-specific expression A;Reference number: 149339; MUID:95340546; PMID:7542241
A;Accession: 149340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIP-1 alpha receptor like-1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: I49340
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                                                                                                                                                                                                                                                                                                                                                                                     R:Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; J. Mol. Biol. 249, 520-528, 1995
A;Title: The DNA sequence of equine herpesvirus 2.
A;Reforence number: S55594; MUID:95302501; PMID:7783207
A;Accession: S55594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-356 < RES>
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Bost Local S
Matches 85
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                                                                                                                    ARTVTEGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFP 183
|||||||:||:|| :|| || || ::: || || :|: |
ARTVTEGVITSIVTWGLAVLAALPEFIFYETEELFEETLCSALYP 188
                                                       NLAISDLEFLLTVPFWAHYAAA--OWDFGNTMCQLLTGLYFIGFESGIFFIILLTIDRYL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSSPIYDI ---- NYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHFP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VTEPSYNTVAKNDFMSGFLCFSINVRAFGITVPTPLYSLVFIIGVIGHVLVVLVLIQHKR
                   NLAISOLLFLLTLPFWMHYIGMYHDWTFGISLCKLLRGVCYMSLYSQVFCIILLTVDRYL
                                                                                                 DVDYEESAPCYKSDTTRLAAQVVPALYLLVFLFGLLGNILVVIIVIRYMKIKNLTNMLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LRNMTSIYLFNLAISDLVFLSTLPFWVDYIMKGDWIFGNAMCKFVSGFYYLGLYSDMFFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.6%;
                                                                                                                                                                           40.0%; Score 449; DB 2;
48.6%; Pred. No. 8.7e-34;
tive 37; Mismatches 51
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Pred. No. 1.5e-37;
                                                                                                                                                                                                                                                                                                                                                                  not shown
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R:Zaballos, A.; Varona, R.; Gutterrez, J.; Lind, P.; Marquez, G.
Blochem. Blophys. Res. Commun. 227, 846-853, 1996
A;Title: Molecular cloning and RNA expression of two new human chemokine receptor-lik
A;Reference number: JC5067; MUID:97040707; PMID:8886020
A;Accession: JC5067
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C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C;Accession: JC5067; G02776; G02387
C;Accession: JC5067; G02776; G02387
                                                                                                                                                                                                                                                                                                                                                                                                                                                         F; 239-260/Domain:
F; 281-304/Domain:
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A;Cross-references: GDB:6053733; OMIM:601834
A;Map position: 3p21-3p21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:045983; NID:91245056; PID:91245057;C:Comment: This protein belongs to the family of beta chemokine receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, January 1996
A;Reference number: H01154
A;Accession: G02387
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F; 239-260/Domain:
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C; Superfamily: vertebrate rhodopsin
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A; Accession: G02776
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A; Residues: 1-355 <ZAB>
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RESULT 13
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F;147-171/Domain:
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A; Residues: 1-355 <NAP>
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                                                         LQCYSFY
                                                                                                                                                                         IFFIILLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLH 175
                                                                                                                                                                                                                    VVCKKLRSITDVYLLNLALSDLLFVFSFPFQTYYLLDQWVFGTVMCKVVSGFYYIGFYSS
                                                                                                                                                                                                                                                                                                                                           MDYQVSSPIYDI-NYY----TSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILIL
                                                                                                                                     MFFITLMSVDRYLAVVHAVYALKVRTIRMGTTLCLAVWLTAIMATIPLLVFYQVASEDGV
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                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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transmembrane #status predicted <TM4>
transmembrane #status predicted <TM5>
transmembrane #status predicted <TM6>
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                                                                                                                                                                                                                                                                                                                                                                                   Score 427.5;
Pred. No. 7.6e
10; Mismatches
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Spinetti, G.; Rocchi, M.; Sani
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probable G protein-coupled receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
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R; Harrison, J.K.;
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C;Keywords: G protein-coupled receptor
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A; Residues: 1-354 <RES>
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A; Accession: I58186
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A;Title: cDNA cloning of a G-protein-coupled receptor expressed A:Reference number: 158186; MUID:94323113; PMID:8047298
                                                                                                                                                                                                                                                                                                                                                                                                                          R;Fan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y. Blochem. Blophys. Res. Commun. 243, 264-268, 1998
A;Title: Cloning and characterization of a novel human chemokine receptor A;Reference number: JC5942; MUID:98139902; PMID:9473515
A;Accession: JC5942
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C;Species: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: JC5942
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C;Superfamily: vertebrate rhodopsin
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A; Residues: 1-344 <FAN>
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                                    136 ALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCS-SHFPYI 185
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                                                                                                                    LFELLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLAVVH-AVF 135
                                                                                                                                                               SEPCOKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYLLNLAISD 76
FSARRRVPCGIITSVLAWVTAILATLPEYVVYKPOMEDQKYKCAFSRTPFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .; Barber, C.M.; 169, 85-89, 1994
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                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                    44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31; Mismatches
                                                                                                                                                                                                                                                   34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 386; DB 2
Pred. No. 5e-28;
                                                                                                                                                                                                                                                                      Score 378; DB 2;
Pred. No. 2.6e-27;
                                                                                   -GDPMCKILIGLYFVGLYSETFFNCLLTVQRYLVFLHKGNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
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                                                                                                                                                                                                                                                                                           Length 344;
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% orphan G protein-coupled receptor - human
N; Alternate names: V28 protein
N; Alternate names: V28 protein
C; Species: Homo sapiens (man)
C; Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                        C;Superianily.
C;Keywords: G protein-coupled receptor.
C;Keywords: G protein-coupled receptor.
F;35-57/Domain: transmembrane #status predicted <TM1>
F;35-57/Domain: transmembrane #status predicted <TM2>
F;104-125/Domain: transmembrane #status predicted <TM4>
F;146-165/Domain: transmembrane #status predicted <TM5>
F;197-217/Domain: transmembrane #status predicted <TM5>
F;197-217/Domain: transmembrane #status predicted <TM5>
F;197-217/Domain: transmembrane #status predicted <TM5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-355 <RAP>
A;Residues: GB:U20350; NID:g665580; PIDN:AAA91783.1; PID:g665581
A;Cross-references: GB:U20350; NID:g665580; PIDN:AAA91783.1; PID:g665581
A;Experimental source: peripheral blood mononuclear cell
C;Comment: This protein is a cell-surface receptor which recognizes extracellular sig C;Comment: This protein is a key regulator of many immune and homeostatic responses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: The orphan G-protein-coupled receptor-encoding A; Reference number: JC4304; MUID:96011651; PMID:7590284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; lymphokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: JC4304
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Best Local
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                                                                                                                                                                             18
                                                                                                                                                                                                                             17 SEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYLLNLAISD 76
                                                                                                                    77
                                                                                                                                                                                                                                                                                                                          Similarity
        LKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFPYI 185
                                                                                               LEFLLTVPEWAHYAAAQWDFGNTMCQLLTGLYFIGFESGIFETILLTIDRYLAVVHAVFA 136
                                                                                                                                                                             LLEVATLPEWTHYLINEKGLHNAMCKETTAFFFIGFFGSIFFITVISIDRYLAIVLAANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                          32.5%;
43.2%;
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Pred. No. 4.3e-26;
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Search completed: June 3, 2003, 15:22:40 Job time: 19.7178 secs

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138

MNNRTVQHGVTISLGVWAAAILVAAPQFMFTK-QKEN---ECLGDYPEV 182

RESULT 15

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2003, 15:09:40 ; Search time 9.85891 Seconds (without alignments) 904.503 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-939-226-6 1122 1 MDYQVSSPIYDINYYTSEPC.....AACHGHLLLGNPKNSASVSK 215

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Databasc : SwissProt_40:*

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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P51685 homo sapien	P56484 mus musculu	P51676 mus musculu	P56492 cercopithec	_		Q9z2i3 cavia porce		P51678 mus musculu	_		P56482 macaca mula	5 mus n	0	ω _	7					P56493 cercopithec			_	097883 hylobates 1					P56439 gorilla gor	pong	P56440 pan troglod	homo sapi	Description

45	44	43	42	41	40	39	38	37	36	35	34
330.5	331.5	331.5	334.5	342.5	345.5	363	365	370	383	386	424
29.5	29.5	29.5	29.8	30.5	30.8	32.4	32.5	33.0	34.1	34.4	37.8
384	352	352	352	378	378	357	355	369	354	354	356
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\sim	_	P30991	-	P47774	·	0	·	•	·	_	097665
homo sapien	macaca mula	homo sapien	cercocebus	mus musculu	homo sapien	homo sapien	homo sapien	mus musculu	mus musculu	rattus norv	macaca mula

ALIGNMENTS

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J. V1rO1. 71:8642-8656(1997).		ds in infection	African	Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.;	mEDLINE=98001387; PubMed=9343222;	SEQUENCE FROM N.A.		Submitted (MAY-1997) to the EMRI/GenBank/DDRI databases	Watanaha M. Doquett N. Garcia D. Garrianati J	V A Doctive II Discribing C., For A., FOWELL E	v Ciacalone I pack powell	Ta Bastide M., Rapian N., Greco T., Touchman J.,	Pariett L., Dedita N., Angari A., Marqis E., Schutz	W.K., Wilson K., Chen E., Gibbs R., Zuo L., Johnson	FROM N.A.		J. Leukoc. B101. 60:147-152(1996).	•	IP-1(alpha), MIP-1(beta), and	"Cloning and functional expression of CC CRES, a human monocyte CC	G T Kanaha	MEDITALE ROOM N.A. DITAGA-BACOLIO.			chemokine receptor (CCR5) for RANTES, MIP-1beta, and	erization of	Ç	MEDLINE-96291862; PubMed-8663314;	SEQUENCE FROM N.A	[2]	CC-chemistry 35:3362-3367/1996)	Molecular cloning and functional expression of a new human	, Vassart G., Parment	MEDLINE-96241590; PubMed-8639485;	SEQUENCE FROM N.A.	[1]	ia; Frimates;	Chordata; Craniata; Vertebrata; E	sapiens (Human).	CCR5 OR CMKBR5.	(HIV-1 fusion co-receptor) (CHEMR13) (CD195 antique).		(Rel. 34,	1996	O15538: O9UPA4:	014700: 014592; 014593; 014595; 014596; 014597; 014598; 014699; 014700: 014701: 014702: 014703: 014704: 014705: 014706: 014707:	HUMAN STANDARD; PRT; 352 AA.	HUMAN	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7

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Zhang L.
Ho D.D.;
"HIV type
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Judoll; PubMed-8649512;
Nagashima K.A., Cayanan C., M-
Paxton W.A.;
HIV-1 entry '
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[7]
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SEQUENCE FROM N.A., AND POLYMORPHISMS.
MEDLINE-98022612; PubMed-9359654;
Zhang L., Carruthers C.D., He T., Huai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.; "The human CC chemokine receptor 5 (CCR5) gene. Mu with 5'-end heterogeneity, dual promoter usage, an polymorphisms within the regulatory regions and no J. Biol. Chem. 272:30662-30671(1997).
                            EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "HIV-1 entry into CD4+ cells CC-CKR-5.";
                                                                                                                     modified and this
                                                                                                                                    use
                                                                                                                                                                                                                                                                                                                                                                                                                                        Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M., Gerard N.P., Gerard C., Sodroski J., Choe H.; "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 381:667-673(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                di Marzio
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Debre P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Identification of a major
                                                                                                                                                                                                                                                     MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL, MAY PLAY A ROLE IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR DIFFERENTIATION. ACTS AS CO-RECEPTOR WITH CD4 FOR PRIMARY NON-SYNCYTIUM-INDUCING STRAINS (NSI) (MACROPHAGE-TROPIC) OF HIV-1 VIRUS. IT PROMOTES ENV-MEDIATED FUSION OF THE VLRUS. SUBCELLULAR LOCATION: Integral membrane protein. TISSUE SPECIFICITY: FOUND IN PROMYELOCYTIC CELLS. PTM: SULFATION CONTRIBUTES TO THE EFFICIENCY OF HIV-1 ENTRY.
                                                                                                                                                                                                            PTM: MODIFIED BY O-LINKED GLYCOSYLATION, GLYCOSYLATION.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PRO
                                                                                                                                                 European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE.
                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         type
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                            U54994;
U57840;
                                                            X91492;
                                                                                       an email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu R., Ellmeier W., Choe S., Unutmaz D., B. O.P., Marmon S., Sutton R.E., Hill C.M., Dav C.C., Schall T.J., Littman D.R., Landau N.R.; Grafton of a maior community.
                                                                                                                                    non-profit institutions as long
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AAC50598.1;
AAB17071.1;
AAB57793.1;
AAC51797.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N.A., AND VARIANT ARG-178
                                                          CAA62796.1;
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                                                                                                                                                                                                             BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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                                                                                                      statement
a license
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G.P., Martin S.R., Huang Y., addon P.J., Koup R.A., Moore J.P.,
                                                                                                                   not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mediated by the chemokine receptor
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                                                                                                                                                                                                                                          OF HIV-1 ENTRY. NOT BY N-LINKED
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 PROSITE; PS00237; G_PROTEIN REPROSITE; PS00237; G_PROTEIN REPROSITE; PS00237; G_PROTEIN REPROSITE; PS50262; G_PROTEIN REPROSITE; PS502622; G_PROTEIN REPROSITE; PS5026222; G_PROTEIN REPROSITE; PS5026222; G_PROTEIN REPROSITE; PS5026222; G_PROTEIN REPROSITE; PS5026222; G_P
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G_PROTEIN_RECEP_F1_2;
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A -> S (IN DBSNP:1800939).

FTIG-VAR_011839.

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                                                                                                                                                                                                                                                                                Edinger A.L., Amedee A., Miller K., Doranz B.J., Endre Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey Peiper S.C., Parmentier M., Broder C.C., Doms R.W.; "Differential utilization of CCR5 by macrophage and T simian immunodeficiency virus strains."; Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
                                                                                                                                                                                                                                                                                                                                                                      Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata;
Mammalla; Euthorla; Primates;
NCBI_TaxID=9598;
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                                                                         SEQUENCE FROM N.A.
MEDLINE-98090115; Pubmed-9430250;
                                                                                                                   Zacharova V., Zachar V., Goustin A.S. "Sequence of chemokine receptor gene HIV type 1 host.";
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          Protet J.-L., Zerblb A., Girard M., Guillet J.-G., Butor C.

"Chimpanzee CXCR4 and CGR5 act as correceptors for HIV type
AIDS Res. Hum. Retroviruses 13:1583-1587(1997).

-I- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO M
MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIG
INCREASING THE INTRACELULUAR CALCIUM IONS LEVEL. MAY PER
IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
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Zacharova V., Zachar V., Goustin A.S.;
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15-JUL-1998 (Rel. 36,
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59 102 EXTRACELLULAR (POTENTIAL).

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54 301 CYTOPLASMIC (POTENTIAL).

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"Sequence evolution of the CCR5 chemokine receptor gene in primates.";
MOI. Biol. Evol. 16:1145-1154(199).
-I- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
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-I- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES. MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES. MINCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. M. IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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Matches 180; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-99416438; pubMed-10486970; Zhang Y.-W., Ryder O.A., Zhang Y.-P.; Zhang Y.-P.; Sheng Y.-P.; Median of the CCR5 chemokine receptor gene in Mol. Biol. Evol. 16:1145-1154(1999).

-I- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO
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Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRHIODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_
PROSITE; PS50262; G_PROTEIN_RECEP_
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobi
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SUBCELULAR LOCATION: Integral membrane protein.
SUMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@fisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE-99416438; PubMed=10486970;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Sequence evolution of the CCR5 chemokine receptor gene in primates.'
MO1. Biol. Evol. 16:1145-1154(1999).
-I- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHI-
MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEYBL. MAY PLAY A ROLE
IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
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30-MAY-2000 (Rel:
15-JUN-2002 (Rel:
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NCBI_TaxID=54133;
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
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SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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illarity 96.2%;
Conservative
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Rel. 41, Last annotation update)
_receptor type 5 (C-C.CKR-5) (CC-CKR-5) (CCR-5).
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39, Last sequence 41, Last annuments
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CYTOPLASMIC (POTENTIAL)
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CYTOPLASHIC (POTENTIAL).

BY SIMILARITY

SULFATION (BY SIMILARITY).

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Pred. No. 4e-52;
6; Mismatches
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AF075448; AAD19860.1; Pro; IPR000276; GPCR_R

PROSITE;

PS00237; G_PROTEIN_RECEP_F1_1; PS50262; G_PROTEIN_RECEP_F1_2; n coupled receptor; Transmembra

Transmembrane;

ransmembrane; Glycoprotein; EXTRACELLULAR (POTENTIAL).

Sulfation

G-protein DOMAIN

TRANSMEM

DOMAIN TRANSMEM

1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL)

(POTENTIAL).

Pfam; PF PRINTS;

PF00001; 71 S; PR00237;

7tm_1; 1. 7; GPCRRHODOPSN

RECEPTORS.

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RESULT 7
CKR5_TRAFR
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Best Local S
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30-MAY-2000
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TRANSMEM
      CCR5 OR CMKBR5
                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                               Trachypithecus francoisi (Francois'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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L5-JUN-2002
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                                                                                                                                                                                                                                                                                                                                      STANDARD;
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39, Last sequence update)
41, Last annotation update)
entor type 5 (C-C CKR-5) (CC
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96.2%;
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CYTOPLASMIC (PC
BY SIMILARITY.
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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3 (POTENTIAL).
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                                                                                                                                                                                                               langur) (Indochinese
ata; Vertebrata; Eutel
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N (BY SIMILARITY).
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CCR5 OR CMKBR5.

Trachypithecus phayrei (Phayre's leaf monkey)

; Metazoa; Eutheria;

Chordata; Primates;

Craniata; V Catarrhini;

Vertebrata; Eutele i; Cercopithecidae;

Euteleostomi;

-CKR-5)

(CCR-5)

(CCR5).

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CKR5_TRAPH
ID CKR5_TRAPH
CKR5_TRAPH
AC 097879;
DT 30-MAY-2000
DT 30-MAY-2002
DE C-C chemoking
GN CCR5 OR CMKBI
OS Trachypithecu
OC Eukaryota; MM
OC Mammalla; Eul
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Best Local S
Matches 177
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DOMAIN
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European Bioinformatics Institute,
by non-profit institutions as 1
fied and this statement is not rem
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PS00237; G_PROTEIN_RECEP_F1_1; 1.

PS50262; G_PROTEIN_RECEP_F1_2; 1.

In coupled receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                            (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 41, Last annotation update)
ne receptor type 5 (C-C CKR-5) (CC-
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CYTOPLASMIC (POTENTIAL).
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SULFATION (BY SIMILARITY).
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CYTOPLASMIC (POTENTIAL).
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4e-52;
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Mol. Biol. Evol. 16:1145-1154(1999).

-I- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
DIFFERENTIATION.
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NCBI_TaxID-61618;
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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HFPY 184
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Pred. No. 4e-52;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
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Zhang Y.-W., Ryder O.
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"Sequence evolution of the CCR5 che
MOI. Biol. Evol. 16:1145-1154(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=61853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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PRODUZI, GPCRHODOPSN.

; PS00237; G_PROTEIN_RECEP_F1_1; 1.

;; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                   MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR
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                                                                                        Macaca Hemover,
Eukaryota; Metazoa; Chordata,
Mammalla; Eutheria; Primates;
Cercopithecinae; Macaca.
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Macaca mulatta (Rhesus macaque),
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
Macaca nemestrina (Pig-tailed macaque)
Macaca nemestrina (Pig-tailed macaque)
Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Margulies B.J., Identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=M.mulatta;
MEDLINE=21354176; PubMed=11461684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Generically divergent strains of "Genetically divergent strains of CCR5 as a coreceptor for entry.";
J. Virol. 71:2705-2714(1997).
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MEDLINE=97213934;
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Newman W., Gerard N.
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MEDLINE-97184592; PubMed-9032394;
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Newman W., Gerard N., Gerard C., Sodroski J.,
"Otilization of C-C chemokine receptor 5 by the envelope
glycoproteins of a pathogenic simian immunodeficiency vii
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7943b; (U4:***,
7943b; (U4:**,
7944b; (U4:**,
                                         SUBCELLULAR LOCATION: Integral r
SIMILARITY: BELONGS TO FAMILY 1
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OF G-PROTEIN COUPLED RECEPTORS.
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(Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 40, Last annotation update)
(Rel. 40, Last annotation update)
ne receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR-5).

RESULT 11 CKR5_PAPHA

CKR5_PAPHA P56441;

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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Comain 1 30 EXTRACELLULAR (POTENTIAL).
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European Bioinformatics Institute. There are no
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Pfam; PF00001; 7tm_1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G_PROTEIN_REC

PROSITE; PS00262; G_PROTEIN_REC

G-protein coupled receptor; Trace

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EMBL; AF105287; AAD20556.1; -.
EMBL; AF105288; AAD20557.1; -.
EMBL; AF105289; AAD20558.1; -.
EMBL; AF105299; AAD20559.1; -.
EMBL; AF023452; AAC63830.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES-P.anubis;
Benton P.A., Timanus D.K., Shearer M.H., Lee.D.R., Kennedy R.C.;
Benton P.A., Timanus D.K., Shearer M.H., Lee.D.R., Kennedy R.C.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
-I- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTERCELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES-P.hamadryas;
MEDLINE-99210133; PubMed-10195758;
Saksena N.K., Wang B., Novembre F.J.,
Species-specific changes in the CCR5
nonhuman primates.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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MEDLINE-97268687; Pu
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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N.A.
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                                                                                                                                                                           G_PROTEIN_RECEP_F1_1; 1.
G_PROTEIN_RECEP_F1_2; 1.
G_PROTEIN_RECEP_F1_2; 1.
receptor; Transmembrane; Glycoprotein;
30 EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (PC
2 (POTENTIAL).
                                                               5 (POTENTIAL)
            EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
                                                  CYTOPLASMIC
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                                                                                        (POTENTIAL)
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.E., Murphey-Corb
                                                                          (POTENTIAL)
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Best Local Sim
Matches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LT 12
CERTO
                                                                                                                                                                                                                                            Chen Z., Gettie A., Ho D.D., Marx P.A.;
"Primary SIVsm isolates use the CCR5 coreceptor in maturally infected in west Africa: a comparison of primary SIVsm, HIV-Z, and SIVmac.";
Virology 246:113-124(1998).
-I- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE.
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062744; 062745; 062746;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
C-C chemokine receptor type 5 (C-C CKR
           EMBL;
EMBL;
                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                       Cercopithecinae;
NCBI_TaxID=9531;
                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                or send an
                                                                                    entities
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                                                                                                                                                                                                                                                                                                                       STRAIN-Isolate 079 MEDLINE-98321155;
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
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                                                                                                                                                                      MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL B INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL, MAY PLAY A IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR DIFFERENTIATION.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTO
          AF051903; 1
AF051903; 1
AF051904; 1
AF051905; 1
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                                                                      and this statement is not removed requires a license agreement (See an email to license@isb-sib.ch).
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551902; AAC39830.1;

551903; AAC39831.1;

551904; AAC39832.1;

551905; AAC39833.1;

FIRO00276; GPCR_Rh
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N-LINKED (GLCNAC. . .) (POT M); 5E1504A9BA1FE8B2 CRC64;
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PRINTS; PR00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.

PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.

PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.

PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
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15-JUL-1998
15-JUL-1998
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NCBI_TaxID=9534;
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EXTRACELLULAR (POTENTIAL)

3 (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)

5 (POTENTIAL)
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Pred. No. 1.7e-51;
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                                                                                                                                                      monkey) (Grivet).
Craniata; Vertebr
                                                                                                                              Catarrhini;
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CKR-5) (CC
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N ISOLATE 079).
                                                                                                                                                        Vertebrata; Euteleostomi;
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CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kuhmann S.E., Platt E.J., Kozak S.L., "Polymorphisms in the CCR5 genes of A implicate specific amino acids in infilmunodefriency viruses.";
                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
TO TYPE CHEMOKINE, BINDS TO
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the European Bioinformatics Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIFFERENTIATION
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sequence of African
                                                                           175;
                                                                                     Similarity
IPR000276; GPCR_Rhodpsn.
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7; GPCRRHODOPSN.
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95.1%;
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| | Jreen monkey CCR-5
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N -> Y.
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Pred. No. 9
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BY SIMILARIT
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of African green monkeys and min
n infections by simian and human
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OF G-PROTEIN COUPLED RECEPTORS
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STRAIN-129;
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15-JUL-1996 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5)
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-C57BL/6, and NIH Swiss; TI
MEDLINE-98001387; PubMed-9343222;
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Eukaryota; Metazoa;
Mammalla; Eutherla;
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                                                                                                                                                                                                                                                                                                                                                   "Polymonn S.E., Platt E.J., Kozak
"Polymorphisms in the CCR5 gene
implicate specific amino acids
immunodeficiency viruses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning and characterization of a novel inflammatory protein-1 alpha receptor."; J. Biol. Chem. 271:14445-14451(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-C57BL/6 X CBA;
MEDLINE-96278910; Publ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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MEDLINE-96205938; PubMed-8631787;
Boring L., Gosling J., Monteclaro
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                                                                                                                                                                                                                                 Doranz B.J.,
                                                                                                                                                                                                                                                     MEDLINE-97404635;
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J. Virol. 71:6305-6314(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecular cloning and functional expression of murine JE (monocyte hemoattractant protein 1) and murine macrophage inflammatory proteinlipha receptors: evidence for two closely linked C-C chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol.
                 B., Kuno K., Harada A., Matsushima K.;
mitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
FUNCTION: RECEPTOR FOR A C-C TYDE CHEMOKINE. BINDS TO
MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SI
INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
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Chem. 271:7551-7558(1996).
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Rodentia;
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Du J.G., Accavitti M.A., Doms R.W.,
mains can mediate coreceptor usage |
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Sciurognathi; Muridae;
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| murine macrophage
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; U47036; AAC52454.1; -.

C; X94151; CAA63867.1; -.

U68565; AAB37273.1; -.

U; U83327; AAC53386.1; -.

U; AF022990; AAC53389.1; -.

U; AF019772; AAB71183.1; -.

U; D83648; BAA12024.1; -.
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                       2
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                                                                                         MDYQVSSP--IYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINC
                                         KRLKSMTDTYLLNLAISDLEFLLTVPFWAHYAAAQWDEGNTMCQLLTGLYFIGFFSGIFF
                     KKLKSVTDIYLLNLAISDLLFLLTLPFWAHYAANEWIFGNIMCKVFTGVYHIGYFGGIFF
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80.1%;
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I -> 
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Pred. No. 1.1e
17; Mismatches
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EXTRACELLULAR
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CYTOPLASMIC ()
6 (POTENTIAL)
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CYTOPLASMIC (F
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CYTOPLASMIC (
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5 (POTENTIAL)
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-> F (IN REF. 2).
-> I (IN REF. 5).
-> Y (IN REF. 3).
-> S (IN REF. 1).
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008556;
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J. Neuroimmunol. 86:1-12(1998).
J. Neuroimmunol. 86:1-12(1998).
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"Cloning of rat HIV-1-chemokine coreceptor CKR5 from microglia and upregulation of its mRNA in ischemic and endotoxinemic rat brain.";
J. Neurosci. Res. 53:16-28(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCR5 OR CMKBR5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-Wistar; TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997
30-MAY-2000
                                                                                                                                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long uselfied and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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MEDLINE-98318173; PubMed-9655467;
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TRANSMEM
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PROSITE; PS00237; GPROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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                                                                                                                                                                                                                                                                                                                              This
                                                                                                                              G-protein
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                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chemokine
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA, MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
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rel. 39, Last annotation update)
receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (MIP-1
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                                                                                                                                  Transmembrane;
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  4 (POTENTIAL).
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5 (POTENTIAL).
                                          CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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1 theropithec
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN 1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
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                 Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammmalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
  SEQUENCE
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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STRAIN=CHCCR5-141A;
Zhang L., Carruthers
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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Pfam; PF00001; 7tm_1; 1.
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Interpro; IPR000276; GPCR.Rhodpsn.
Pfam; PF00001; 7tm.1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primatcs; Catarrhini; Hylobatidae; Hylobates.
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SEQUENCE
Mueller-Trutwin M.C., Corbet S., Hansen J., Diop O., Georges-Courbot M.-C., Barre-Sinoussi F., Fomsgaard A.; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases-EMBL; AF035214; AAD44007.1; -. InterPro; IPR000276; GPCR_Rhodpsn. Pfam; PF00001; 7tm_1; 1. PRINTS; PR00237; GGPCRRHODDPSN. PRINTS; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                        MEDLINE-99335215; PubMed-10408730; Mailer-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.C., Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.; "Mutations in CCR5-coding sequences are not associated with SIV carrier status in African nonhuman primates."; AIDS Res. Hum. Retroviruses 15:931-939(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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*Species-specific changes in the CCR5 gene fron nonhuman primates. ";
AIDS Res. Hum. Retroviruses 15:479-483(1999).
EMBL: AF105291; AAD20560.1; -
EMBL: PR00021-276; GPCR_Rhodpsn.
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PROSITE: PS50262; G_PROTEIN_RECEP_F1_2;
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Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                    40578
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of the
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96.2%;
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Pred.
                                                                                                                                                                                                                                                                                                                     6;
                                                                                                                                                                                                                                                                                                                                          Score 938;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                    4366F149C3B4938F CRC64;
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No. 1
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L.3e-79;
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Q9MZA3;
01-OCT-2000
01-OCT-2000
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CC_chemokine
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01-DEC-2001
01-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                        Hylobates agilis unko.
Hylobates agilis unko.
Eukaryota; Metazoa; Chordata;
Eukaryota; Metazoa; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor.
SEQUENCE
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Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF177883; AAK43366.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. zhang Y., Ryder O.A.,
                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9MZA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
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DEC-2001 (TREMBLIGEL 1)
MAR-2002 (TREMBLIGEL 2)
Chemokine receptor 5.
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177; Conserv
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TE; PS00237; G_P
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; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
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96.2%;
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Catarrhini;
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i; Hylobatidae; Hylobates.
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L.3e-79;
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                                                                                                                                                                                               E., Feuillet P.M., A.J., Murthy K.K.,
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J. Biol. Chem. 275:18946-18951(2000).
EMBL; AF252551; AAR87981.;
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR000237; GPCRRHODDPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequence evolution of chemokine receptor CCR5 Submitted (JUN 1998) to the EMBL/GenBank/DDBJ d EMBL; APO75447; AAD19859.1; ... EMBL; AF075444; AAD19856.1; ... Interfero; IPR000276; GPCR_Rhodpsn. Pfam; PF00001; 7tm_1; 1. PRINTS; PR00027; GPCRRHODDSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pygathrix avunculus (Tonkin snub-nosed monkey), and Pygathrix roxeliana (golden snub-nosed monkey). Pygathrix roxeliana (golden snub-nosed monkey). Euteleostomi; Eukaryota, Mctazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
C-C chemokine receptor type 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00237;
PROSITE; PS50262;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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NCBI_TaxID-66062,
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G_PROTEIN_RECEP_F1_2;
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95.7%;
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Pred. No. 2.
                                                                                                                                                                                                                                                                                                                     Score 935; DB 6;
Pred. No. 2.5e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                              037CFA9E12E532F3 CRC64;
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Spearman P.W., Mburu D.N., Graham B.S.;

Polifierential Utilization of CCR5 Molecules from Three East

Simian Species by the HIV-1 Envelope Glycoprotein.";

Submitted (APR-199) to the EMBL/GenBank/DDBJ databases.

R EMBL; AF141639; AAD32684.1; ".

R InterPro; IPR000276; GPCR_Rhodpsn.

R Pfam; PF000017; Tfm_1; 1.

R PRINTS; PR00237; GPCRRHODOPSN.

R PROSITE; PS00237; GPROTEIN_RECEP_F1_1; UNKNOWN_1.

R PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
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01-NOV-1999
01-DEC-2001
                             Nasalis larvatus (Proboscis monkey)
Eukaryota; Metazoa; Chordata; Crani
Mammalia; Eutheria; Primates; Catar
                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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Mammalia; Eutheria;
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ta; Metazoa; Chordata; Craniata; Vertebrata; Eutele
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llarity 95.7%;
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Pred. No. 3.1e-79
6; Mismatches
                             Craniata; Vertebrata;
Catarrhini; Cercopith
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                             Colobinae;
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Zhang Y., Ryder O.A., Zhang Y.;
"Sequence comparison of the CCR5 gene in primates and primate phylogeny.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF17882; AAK43365.1;
EMBL; AF17882; AAK43365.1;
InterPro; IPR000276; GPCR_KhodpSn.
Pfam; PF00001; 7tm_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
C-C chemokine receptor 5.
                                                                                                                                                                                                                                                                                                                                                                                        Q95NC3
                                                                                                                                                                                                            SEQUENCE FROM N.A., Zhang Y.; Zhang Y.; Zhang Y., Ryder O.A., Zhang Y.; Sequence comparison of the CCR5 gene in primates and primate phylogeny.
                                                                                                                                                                                                                                                                       Miopithecus talapoin (Talapoin) (Cercopithecus talapoin).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Miopithecus.
                                                                                                                                                                                                                                                                                                                                                                             Q95NC3;
                                                                                                                                                           Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF177886; AAK43369.1; -
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                          Receptor
                                                                                                                                     prosite; ps00237; G_protein_recep_f1_1;
prosite; ps50262; G_protein_recep_f1_2;
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                                                                               Local Similarity
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                        LKSMTDIYLLNLAISDLFFLLTVPEWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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                                                                     Conservative
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96.2%;
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Last annotation update)
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Pred. No. 3.1e-79;
7; Mismatches 1
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                                                                        Mismatches
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                                                                    DB 6;
J.1e-79;
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018770;
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NON_TER
SEQUENCE
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF011538; AAB65738.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
pfam; pF00001; /tm_1; 1.
pRINTS; PR00237; GPCRHODOPSN.
pROSITE; pS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1
pROSITE; pS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhang_L., Carruthers C.D., He T., Huang
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STRAIN-MACCR5-140A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ho D.D.;
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352 AA;
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Pred. No. 3.8e-79;
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Perfect score:
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1: /cgn3_6/ptodata/1/paa/U

2: /cgn3_6/ptodata/1/paa/U

3: /cgn4_6/ptodata/1/paa/U

4: /cgn2_6/ptodata/1/paa/U

5: /cgn2_6/ptodata/1/paa/U

6: /cgn2_6/ptodata/1/paa/U

7: /cgn2_6/ptodata/1/paa/U
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 259
LENGTH: 352
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Best Local Similarity 100.0%;
Matches 352; Conservative (
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APPLICANT:
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TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-002710PC
CURRENT APPLICATION NUMBER: PCT/US02/29560
CURRENT FILING DATE: 2025-11-01
PRIOR APPLICATION NUMBER: US 60/323,469
PRIOR FILING DATE: 2001-09-17
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: Gish, Kurt C.
: Hevezi, Peter A.
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   SOFTWARE: Patentin
SEQ ID NO 1
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                                                                                CURRENT APPLICATION NUMBER: PCT/US03/03763
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 10/071,866
PRIOR EILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 10/072,301
PRIOR FILING DATE: 2002-02-08
                                                  PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2002-04-25
                                                                                                                                                                                           APPLICANT: Hua, Shaobing
APPLICANT: Pauling, Michelle H.
APPLICANT: Zhu, Li
TITLE OF INVENTION: METHODS FOR GENERATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Progenics Pharmaceuticals, Inc. TITLE OF INVENTION: Sulfated CCR5 Peptides FILE REFERENCE: 61010-AB1-PCT/JPW/JTL
                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: PCT/CURRENT FILING DATE: 2002-02-28 NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
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Pred. No. 2.5e-171;
Mismatches 0;
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US-09-949-002-303
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SEQ ID NO 303
LENGTH: 352
TYPE: PRT
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Best Local (
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CURRENT FILING DATE: 2000-01-28
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, N
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
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Pred. No. 2
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Pred. No. 2.5e-171;
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2.5e-171;
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Sequence 1, Application US/10086814
GENERAL INFORMATION:
APPLICANT: Dragle, Tatjana
APPLICANT: Olson, William C.
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FO:
FILE REFERENCE: 61010-AB-1
CURRENT APPLICATION NUMBER: US/10/086,814
CURRENT FILLNG DATE: 2002-02-28
NUMBER OF SEQ ID NOS: 38
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US-09-949-004-242
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US-09-949-004-242
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Graig et al.
TITLE OF INVENTION: POLYMORPHISMS IN HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTOR GENES ASSOCIATED WITH DISEASE,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000848
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US/09/949,004
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: 60/232,045
PRIOR FILING DATE: 2000-09-13
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Best Local
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SOFTWARE: FABLSEQ for Windows Version
IEQ ID NO 242
LENGTH: 352
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Pred. No. 2.5e-171;
D; Mismatches 0;
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                                                                                                               PRIOR APPLICATION NUMBER: US 60/323,469
PRIOR FILING DATE: 2001-09-17
PRIOR PELICATION NUMBER: US 60/323,887
PRIOR FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: US 60/325,114
PRIOR PELING DATE: 2001-09-25
PRIOR PELICATION NUMBER: US 60/340,944
PRIOR FILING DATE: 2001-10-29
PRIOR PELICATION NUMBER: US 60/350,666
PRIOR PELICATION NUMBER: US 60/350,666
PRIOR PELICATION NUMBER: US 60/355,145
PRIOR PELICATION NUMBER: US 60/355,145
PRIOR APPLICATION NUMBER: US 60/355,257
PRIOR PELICATION NUMBER: US 60/355,257
PRIOR PELICATION NUMBER: US 60/355,257
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60, PRIOR FILING DATE: 2002-04-04 PRIOR APPLICATION NUMBER: US 60, PRIOR FILING DATE: 2002-04-12 NUMBER OF SEQ ID NOS: 412 SOFTWARE: FASTSEQ for Windows VaseQ ID NO 259
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   SOFTWARE:
SEQ ID NO 2
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CURRENT FILING DATE: 2002-12-13
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TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions
TITLE OF INVENTION: Methods of Screening for Modulators of Cance
FILE REFERENCE: 018501-002710US
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ORGANISM:
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Gish, Kurt C.
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US-10-245-882-259
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APPLICANT: Olson, William
APPLICANT: Olson, William
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/61010-1/JFW/MAF/DJK
CURRENT APPLICATION NUMBER: US/10/323,314
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
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Best Local (
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Best Local
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TYPE: PRT
ORGANISM: human
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Pred. No. 2.5e-171;
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TITLE OF INVENTION: Methods and Compositions fo
TITLE OF INVENTION: Urological Disorders Using
FILE REFERENCE: MPIO1-289PIRM
CURRENT APPLICATION NUMBER: US/10/290,058A
CURRENT FILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: 60/344,552
PRIOR APPLICATION NUMBER: 60/344,552
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-290-058A-6
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US-10-225-567A-352
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US-10-225-567A-352
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GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
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Best Local Similarity
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APPLICANT: BUTMER, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES
FILE REFERENCE: 1920-4-4
                                                                                                                                                                 APPLICANT: Silos-Santiago,
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PRIOR FILING DATE: 2000-12-19
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TYPE: PRT
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CURRENT APPLICATION NUMBER: US/10/360,828
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 10/071,866
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 10/072,301
PRIOR PILING DATE: 2002-02-08
PRIOR PILING DATE: 2002-04-08
PRIOR FILING DATE: 2002-04-25
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PATENTIN VCTS1ON 3.1
SEQ ID NO 1
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US-10-360-828-1
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US-10-290-058A-6
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LENGTH: 35
TYPE: PRT
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Best Local S
                                                                                                                                                 Matches
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TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
FILE REFERENCE: 25636-727
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ORGANISM: Homo sapiens
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Pred. No. 2.5e-171;
Mismatches 0;
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Pred. No. 2.5e-171;
; Mismatches 0;
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OTHER INFORMATION:
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US-10-239-423-67
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GENERAL INFORMATION:
APPLICANT: FORSSMANN, Wolf-Georg; FORSSMANN, Ulf; ADERMANN, Knut;
APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikolaj
TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells at TITLE OF INVENTION: For Treating Tumor Diseases and Inflammatory Diseases,
TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine
TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction Current Application NUMBER: US/10/239,423
CURRENT APPLICATION NUMBER: US/10/239,423
BRIOR ADSTRANTON NUMBER: DE002-09-23
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Best Local Similarity
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PRIOR APPLICATION NUMBER: DEL0016013.1
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 84
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TYPE: PRT
ORGANISM: Artificial Sequence
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             GEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISVGL 352
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RESULT 13

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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WIT:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WIT:
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DI
FILE REFERENCE: CL001456
CURRENT PAPPLICATION NUMBER: US/60/453,135
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7850
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US-60-452-680-12568
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TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF 1
FILE REFERENCE: CL001450
CURRENT APPLICATION UNMERS: US/60/452,680
CURRENT FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 116213
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12568
LENGTH: 352
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Seguence 12568, Application
GENERAL INFORMATION:
APPLICANT: CARGILL, Michel
APPLICANT: GRUDE, Andrew
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US-60-453-135-7850
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US-60-453-135-7850
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: IAKOUBOVA, Olga
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                                                             Score 1841; DB 7;
Pred. No. 2.5e-171;
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US-60-453-050-7850
; Sequence 7850, Applic
; GENERAL INFORMATION:
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US-60-453-050-7850
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APPLICANT: LUKE, May
APPLICANT: LUKE, May
APPLICANT: LUKE, May
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
TITLE REFERENCE: CLO01457
CURRENT APPLICATION NUMBER: US/60/453,050
CURRENT APPLICATION NUMBER: US/60/453,050
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7850
LEMGTH: 352
TYPE: PRT
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MIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFV
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Search completed: June Job time: 80.2222 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                             Score
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seq length: 2000000000
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/cgn2_6/ptodata/1/paa/US087_COMB.pep:*
/cgn2_6/ptodata/1/paa/US088_COMB.pep:*
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/cgn2_6/ptodata/1/paa/US093_COMB.pep:*
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/cgn2_6/ptodata/1/paa/US06_C
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/cgn2_6/ptodata/1/paa/US084_COMB.pep:*
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/cgn2_6/ptodata/1/paa/US102_COMB.pep:*
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/prodata/1/paa/US095_COMB.pep:*
/prodata/1/paa/US096_COMB.pep:*
/prodata/1/paa/US097_COMB.pep:*
US-09-626-500-6

US-09-626-939-6

US-09-938-703-6

US-09-938-719-6

US-09-939-726-6

US-60-182-562-1416
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equence 2,	uence 84	equence 2, Appl	22	equence 1,	equence 2,	e 1, Appl	equence 1, Appl	equence 22, App	Sequence 5, Appl1	e 5, Appl	equence 5, Appl	equence 477, Ap	e 15, App	equence 1, Appl	equence 22,	equence 22, App	equence 2, Appl	equence 14, App	O	o 5,	e 5,	e 2	N '	დ გ	'n	e 4, App	e 2, App	ce 2,	equence 22,	equence 3,	equence 1	e 22, App	22, App	4, App	4	equence 4, App	4, App	Sequence 4, Appli

ALIGNMENTS

US-09-62-500-6

Sequence 6, Application US/09626500

GENERAL INFORMATION:
APPLICANT: SANSON, MICHEL
APPLICANT: WASSART, GILBERT
APPLICANT: VASSART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
TOTHE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
TITLE OF INVENTION:
APPLICATION SEQUENCE: 17
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIU

US-09-626-500-6

MOLECULE TYPE: protein

Indels Length 215;

0

Gaps

____ aminc acid TOPOLOGY: line

INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:

215 amino acids

FILING DATE: ATTORNEY/AGENT INFORMATION:

NAME: Altman, Daniel E REGISTRATION NUMBER: 34 REFERENCE/DOCKET NUMBER:

Daniel E 34,115

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Best Local Similarity
Matches 215; Conserv
REPERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SAMSON, MICHEL
APPLICANT: PARMENTIER, MARC
APPLICANT: VASSART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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                                                                                                                                                                                  FILING DATE:
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                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
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RESULT 3
US-09-938-703-6
US-09-938-703-6
; Sequence 6, Application US/09938703
; GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
PARMENTIER, MARC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: US-09-626-939-6
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Best Local S
Matches 215
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                                                                                                Best Local Similarity
Matches 215; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION NUMBER: US/09/938,703
FILING DATE: 24-Aug-2001
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
OCCUPANTION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens,
STREET: 620 Newport Center |
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LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 09/626,939 FILING DATE: 2000-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Newport Beach
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: <Unknown>
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                                                                                                       100.0%; Score 1122; DB 23; 100.0%; Pred. No. 1.5e-103; rive 0; Mismatches 0;
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Pred. No. 1.5e-103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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TOPOLOGY: Inear
HOLECULE TYPE: Protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-938-719-6
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US-09-938-719-6
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GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 09/626,939
FILING DATE: 27-JULY-2000
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,719
FILING DATE: 24-Aug-2001
CLASSIFICATION: -CURROWND
PRIOR APPLICATION DATA:
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LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
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181
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                                                                                                 61 LKSWTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
                                                                                                                                                                                                                                    1 Similarity
215; Conserv
                                                                                                                                                                           1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
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                                                                                                                                                         MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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STATE: CA
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llarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                    Score 1122; DB 23;
Pred. No. 1.5e-103;
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US-09-939-226-6
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; Sequence 1416, Application US/60182562
                  RESULT 6
US-60-182-562-1416
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APPLICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
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ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
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LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
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                                                                                                                   HFPYIKDSHLGAGPAAACHGHLLLGNPKNSASVSK 215
                                                                                                                                                                                              LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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                                                                                               HFPYIKDSHLGAGPAAACHGHLLLGNPKNSASVSK 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 215 amino acids TYPE: amino acid
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1416
LENGTH: 191
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Best Local Similarity
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REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: 4:
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CURRENT FILING DATE: 2000-02-15
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ITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
ITLE OF INVENTION: PROTEINS, AND USES THEREOF
                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                     ATTORNEY/AGENT INFORMATION: NAME: Altman, Daniel E
                                                                                                                          CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
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                                   NAME: Altman, Daniel E
REGISTRATION NUMBER: 34
                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                           FILING DATE:
                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                FILING DATE:
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T: 620 Newport Center Drive
Newport Beach
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                                                                                                                                                                                                                                                                    Floppy disk
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ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
ACTIVE AND NUCLEIC ACID MOLECULES ENCODING SAID R
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99.0%;
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                                     34,115
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Pred. No. 2.4e
0; Mismatches
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Drive 16th Floor
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                                                       ; MOLECULE TYPE: protein US-09-626-939-4
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Query Match
Best Local Similarity
Matches 184; Conserv
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Best Local Similarity
                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATING TOSTEM: PC-DOS_MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 92660
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                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                 LENGTH:
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LIBERT, FREDERICK
VENTION: ACTIVE AND INACTIVE CC-CHEMOKINES
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   Conservative
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O Newport Center Drive 16th Floor
                                                                                                                                                                                     Daniel
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100.0%;
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Pred. No.
          Score 958; DB 20;
Pred. No. 3.3e-87;
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   Mismatches
                                                                                                                                                                                                                                                                                                                       Version
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RESULT 9
US-09-938-703-4
; Sequence 4, Application US/09938703
; GENERAL INFORMATION:
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Best Local Similarity
Matches 184; Conserv
                                                                                                                                                                                                                                                                                                                                          NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,703
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
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MEDIUM TYPE: Floppy disk
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VASSART, FREDERICK
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION UMBER: 09/626,939
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
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                                                    LKSMTDIYLLNLAISDLFELLTVPFWAHYAAAQWDFGNTMCQLLTGLYEIGFESGIFFII 120
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   LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                                   LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII
                                                                                                                                                                                                                                                                                           LENGTH: 184 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                        Conservative
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                                                                                                                                                                     85.4%; Score 958; DB 23;
100.0%; Pred. No. 3.3e-87;
vative 0; Mismatches 0;
                                                                                                                                                                                                       Length 184;
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RESULT 10
US-09-938-719-4
Sequence 4, Application US/09938719
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 09/626,939
FILING DATE: 27-JULY-2000
ATTORNEY_AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                         Matches 184;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
CORRESSEE: Knobbe, Martens, Olson & Bear
ADDRESSEE: 620 Newport Center Drive 16th Floor
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TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR

AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                         Similarity
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FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
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                                HFPY 184
                                                                                                                                                                                                       MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acids
                                                                                                                                     LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII
                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
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                                                                                                                          Sequence 22, Application PC/TUS0104152A GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                    APPLICANT: Human Genome Sciences, Inc APPLICANT: Rosen, Craig A.
                                            APPLICANT:
                                                               APPLICANT:
                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION: -Unknown>
OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
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AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
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REGISTRATION NUMBER: 34,115
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                                                          Rosen, Craig A.
Roschke, Victor
                       Ruben, Steven
                                          Li, Yi
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100.0%; Pr
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; LENGTH: 352
; TYPE: PRT
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Best Local :
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PRIOR APPLICATION NUMBER: US 60/181,258
PRIOR FILING DATE: 2000-02-09
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SOFTWARE: PatentIn version 3.0
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PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 58
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CURRENT FILING DATE: 2001-02-09
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Pred. No. 6.7e-87;
Pred. No. 6.7e-87;
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; SOFTWARE: Patent
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
PCT-USO1-06699-1
APPLICANT: KILCM, Stefanie E.
APPLICANT: KOSNY, Becna
TITLE OF INVENTION: Haplotypes of the CCR5 Gene
FILE REFERENCE: MWH-0505CT CCR5
CURRENT APPLICATION NUMBER: PCT/US01/10708
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/194,361
PRIOR FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapien
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GENERAL INFORMATION:
APPLICANT: Genalseance Pharmaceuticals
APPLICANT: Choi, Julie
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Best Local Similarity
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TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/61010-A-PCT/JPW/SHS/AX
CURRENT APPLICATION NUMBER: PCT/US01/06699
CURRENT FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 17
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Search completed: June
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Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/1/paa/U

2: /cgn2_6/ptodata/1/paa/U

3: /cgn2_6/ptodata/1/paa/U

4: /cgn2_6/ptodata/1/paa/U

5: /cgn2_6/ptodata/1/paa/U

6: /cgn2_6/ptodata/1/paa/U

7: /cgn2_6/ptodata/1/paa/U
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1 MDYQVSSPIYDINYYTSEPC.....AACHGHLLLGNPKNSASYSK 215
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           GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd
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/cgn^2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
/cgn^2_6/ptodata/1/paa/US01_NEW_COMB.pep:*
/cgn^2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
/cgn^2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
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1 PCT-USO3-03745-1
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1 SUS-09-949-002-303
5 US-09-949-004-242
6 US-10-245-882-259
6 US-10-245-882-259
6 US-10-225-667A-352
6 US-10-233-314-1
6 US-10-239-058A-6
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-949-004-44	-466-412-7	US-60-465-241-4290	-455	US-60-453-050-7701	US-60-453-135-7701	US-60-452-680-12373	US-10-219-051B-10296	US-10-219-051B-10292	US-10-239-423-63	US-09-893-512A-13	49-	US-60-466-412-7700	US-60-465-241-4289	US-60-455-444-4289	0-453-050-	US-60-453-135-7700	US-60-452-680-12372	US-10-239-423-64
Sequence 443, App	Sequence 7701, Ap	Sequence 4290, Ap		Sequence 7701, Ap	æ	Sequence 12373, A	Sequence 10296; A	1029	63,	•••	244	Φ	Sequence 4289, Ap		e 77	Sequence 7700, Ap	e 12372,	Sequence 64, Appl

ALIGNMENTS

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RESULT 2	Oy 181 HFPY 184	OY 121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSOKEGLHYTCSS 180	Qy 61 LKSMTDIYLLNLAISDLEFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFESGIFFII 120 	Qy 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60	Query Match 85.4%; Score 958; DB 1; Length 352; Best Local Similarity 100.0%; Pred. No. 3.2e-88; Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	; PRIOR FILING DATE: 2001-09-17; NUMBER OF SEQ ID NOS: 412; SOFTWARE: FRATSEQ for Windows Version 3.0; SEQ ID NO 259	CURRENT APPLICATION NUMBER: PCT/US02/29560 CURRENT FILING DATE: 2025-11-01 PRIOR APPLICATION NUMBER: US 60/323,469	TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and TITLE OF INVENTION: Methods of Screening for Modulators of Cancer the FILE REFERENCE: 018501-002710PC		; APPLICANT: ATAT, DANIEL ; APPLICANT: ATAT, Natasha ; APPLICANT: Gish, Kurt C. ; APPLICANT: Hevezi, Peter A.	0.00	

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; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-03763-1
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PCT-US02-06345-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application PC/TUS0303763 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Progenics Pharmaceuticals, Inc., TITLE OF INVENTION: Sulfated CCR5 Peptides FILE REFERENCE: 61010-AB1-PCT_IPM/JTL CURRENT APPLICATION NUMBER: PCT/US02/06345 CURRENT FILING DATE: 2002-02-28
                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.1 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 10/071,866
PRIOR ETLING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 10/072,301
PRIOR ETLING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 10/133,978
PRIOR ETLING DATE: 2002-04-25
NUMBER: US 10/133,978
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                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: PCT/US03/03763
CURRENT FILING DATE: 2003-02-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Pauling, APPLICANT: Zhu, Li
                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITLE OF INVENTION: METHODS FOR GENERATING ANTIBODIES AGAINST MEMBRANE PROTEINS ILE REFERENCE: 25636-728
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184;
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                                                                                  MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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                                                                                                                               85.4%; Score 958; DB 1; milarity 100.0%; Pred. No. 3.2e-88; Conservative 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000790
FILE REFERENCE: CL000790
FILE REFERENCE: CL000790
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SEQ ID NO 303
LENGTH: 352
                                                                                                                                GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN HUMAN G-PROTEIN COUPLED

TITLE OF INVENTION: RECEPTOR GENES ASSOCIATED WITH DISEASE,

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: CL000848

CURRENT APPLICATION NUMBER: US/09/949,004

CURRENT FILING DATE: 2002-12-20

PRIOR APPLICATION NUMBER: 60/232,045

PRIOR FILING DATE: 2000-09-13
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Best Local Similarity
                                                     NUMBER OF SEQ ID NOS: 6961
SOFTWARE: FRATSEQ for Windows Version 4.0
SEQ ID NO 242
LENGTH: 352
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CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
ORGANISM: Human
-09-949-004-242
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100.0%;
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APPLICANT: Drag1c, Tatjana
APPLICANT: Olson, William C.
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FO
FILE REFERENCE: 61010-AB-1
CURRENT APPLICATION NUMBER: US/10/086,814
CURRENT FILING DATE: 2002-02-28
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patchtin version 3.1
SEQ ID NO 1.
                                                                                                                                                                                                                                                                                        RESULT 7
US-10-245-882-259
Sequence 259, Application US/10245882
GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-086-814-1
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US-10-086-814-1
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Best Local Similarity
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Bost Local Similarity
                                                                                                                                                                 APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natas
APPLICANT: Gish, Kurt
APPLICANT: Hevezi, Pet
                                                                        APPLICANT:
                                                                                                                                APPLICANT:
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   Aziz, Natasha
Gish, Kurt C.
Hevezi, Peter A.
Mack, David H.
Wilson, Keith E.
Zlotnik, Albert
Eos Biotechnology, I
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             of Cancer,
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                                                                       ; TYPE: PRT
; ORGANISM: human
US-10-323-314-1
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US-10-245-882-259
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PRIOR FILING DATE: 2001-09-17
PRIOR FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: US 60/323,887
PRIOR PRIOR APPLICATION NUMBER: US 60/325,114
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR APPLICATION NUMBER: US 60/355,145
PRIOR APPLICATION NUMBER: US 60/355,145
PRIOR APPLICATION NUMBER: US 60/355,257
PRIOR APPLICATION NUMBER: US 60/355,257
PRIOR APPLICATION NUMBER: US 60/369,899
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                                                                                                                                                                                                      Sequence 1, Application US/10323314
GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/651010-1/JPW/MAF/DJK
CURRENT APPLICATION NUMBER: US/10/323,314
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 17
                                                                                                                                   SOFTWARE: PatentIn
SEQ ID NO 1
LENGTH: 352
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LENGTH: 352
  Query Match
Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/245,882
CURRENT FILING DATE: 2002-12-13
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TYPE: PRT
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; Pred. No. 3.2e-88;
0; Mismatches 0;
Score 958; DB 6; pred. No. 3.2e-88
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US-10-225-567A-352
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Best Local S
Matches 184
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    Sequence 6, Application US/10290058A

GENERAL INFORMATION:
APPLICANT: Silos-Santiago, Inmaculada
PITLE OF INVENTION: Methods and Compositions for Treating
PITLE OF INVENTION: Urological Disorders Using 313, 333,
PITLE REFERENCE: MPIO1-289PIRM
CURRENT FILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: US/10/290,058A
CURRENT FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/344,552
PRIOR FILING DATE: 2001-11-07/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REPERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LifeSpan Biosciences APPLICANT: Brown, Joseph P.
                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1 
;EQ ID NO 352 
LENGTH: 352
                                                                                                                           -10-290-058A-6
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Similarity 100.0%;
84; Conservative 0
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SEQ ID NOS:
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-290-058A-6
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CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 10/071,866
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 10/133,978
PRIOR FILING DATE: 2002-04-25
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin version 3.1
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LENGTH: 352
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Matches 18
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GENERAL INFORMATION:
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Best Local
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LENGTH: 352
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Best Local Similarity
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TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES
FILE REFERENCE: 25636-727
                                                                                                                                                                                                                                                                         TYPE: PRT
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                                                                           LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                     HFPY 184
                                          HFPY
                                                               LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS
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Pred. No. 3.2e-88
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US-10-239-423-67; Sequence 67, Application US/10239423; GENERAL INFORMATION:
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OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-67
                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-452-680-12568
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US-60-452-680-12568
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Best Local Similarity
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Best Local
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APPLICANT: GRUPE, Andrew
TITLE OF INVENTION: GREFTIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001450
CURRENT FILING DATE: 2003-03-07
CURRENT FILING DATE: 2003-03-07
RUMBER OF SEO ID NOS: 116213
SOFTWARE: FBSLSEQ for Windows Version 4.0
SEQ ID NO 12568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the TITLE OF INVENTION: Cell Surface Protecme of Tumor and Inflammation Cells TITLE OF INVENTION: Cell Surface Protecme and Inflammatory Diseases and Inflammatory Diseases.

TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-0
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                               ENGTH: 352
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MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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                                      85.4%; Score 958; DB 7; I
100.0%; Pred. No. 3.2e-88;
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100.0%; Pred. No. 3.2e-88;
O. Mismatches 0;
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; SEQ ID NO 7850
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-135-7850
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US-60-453-050-7850
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Matches
                              SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 7850 LENGTH: 352
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TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS C
                                                                                                 CURRENT APPLICATION NUMBER: US/60/453,050 CURRENT FILING DATE: 2003-03-10
                                                                                                                                  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION A FILE REFERENCE: CL001457
                                                                                                                                                                                      APPLICANT: CARGILL, Michele APPLICANT: LUKE, May
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/60/453,135
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
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                                                                                   NUMBER OF SEQ ID NOS: 82762
ORGANISM:
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Search o Job timo	Qу	Db Qy	ф	Qy	US-60-453-050 Query Match Best Local Matches 18
Search completed: June 3, 2003, 15:33:14	181 HFPY 184	121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180	61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120	1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60	US-60-453-050-7850 US-60-453-050-7850 85.4%; Score 958; DB 7; Length 352; Query Match Best Local Similarity 100.0%; Pred. No. 3.2e-88; Best Local Similarity 100.0%; Pred. No. 3.2e-88; Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Job time : 47.7778 secs					